

PT	- esp. useful as blood plasma expanders.	PD	01-MAY-1990.
XX	Disclosure; fig 2; 20pp; English.	XX	XX
PS		PF	26-OCT-1988; 88JP-0268302.
XX	Mature protein of human serum albumin (see corresp. AAN0128).	XX	XX
CC	Used to make new N-terminal fragments which are used as plasma	PR	26-OCT-1988; 88JP-0268302.
CC	expanders, or as substitutes for HSA or BSA, in tissue culture	XX	XX
CC	media	PA	(TOFU) TOS NENRYO KOGYO KK.
CC	(Updated on 25-MAR-2003 to correct PA field.)	XX	PA
XX		DR	WPI: 1990-176228/23.
SO	Sequence 585 AA;	DR	N-PSDB; AQQ04719.
XX	Human serum albumin Prepn. by yeast host -	XX	
Query	Score 3103; DB 10; Length 585;	PT	by culturing transformed plasmid yeast to produce serum, and
Best Local Similarity 100.0%; Pred. No. 9.5e-255;	PT	removing it.	
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
QY	1 DAHKSEYAHFRKFDLGEENFKALVLAQYLQOCPEFDHVLYNEVTEFAKTCVADSEAE 60	PS	Disclosure; Page ?; ?pp; Japanese.
Db	1 DAHKSEYAHFRKFDLGEENFKALVLAQYLQOCPEFDHVLYNEVTEFAKTCVADSEAE 60	XX	
QY	61 NCDKSLTLEFDKLTQVLRLETVGENADCCAKQPERNECELOHKDNPNPRLVPEV 120	CC	Mature HSA-A may be produced using the sequence incorporated into a
Db	61 NCDKSLTLEFDKLTQVLRLETVGENADCCAKQPERNECELOHKDNPNPRLVPEV 120	CC	plasmid vector with suitable controllers, and transferred to a yeast
QY	121 DYMCTAHDNEETFKLTYETARRHPPYTAPELLFFAKRYKAFTCCQADRACLLP 180	CC	expression system.
Db	121 DYMCTAHDNEETFKLTYETARRHPPYTAPELLFFAKRYKAFTCCQADRACLLP 180	XX	
QY	181 KLDLRLDEKASSAKQURKCAASLQKFGERAKVARYARLQSOPKKAFAEYSKLVTDLK 240	SO	Sequence 585 AA;
Db	181 KLDLRLDEKASSAKQURKCAASLQKFGERAKVARYARLQSOPKKAFAEYSKLVTDLK 240	Query Match 100.0%; Score 3103; DB 11; Length 585;	
QY	241 VHTECCHGDLLECADDRADLAKYICENODSSKLKECEKPLLEKHCIAEVENDEPA 300	Best Local Similarity 100.0%; Pred. No. 9.5e-255;	
Db	241 VHTECCHGDLLECADDRADLAKYICENODSSKLKECEKPLLEKHCIAEVENDEPA 300	Mismatches 0; Indels 0; Gaps 0;	
QY	301 DLPSLAADFVESDKWNKAAXDVLGMFLYETARRHEDYSYVLLRLAKTYETTLER 360	Matches 585; Conservative 0;	
Db	301 DLPSLAADFVESDKWNKAAXDVLGMFLYETARRHEDYSYVLLRLAKTYETTLER 360	QY	1 DAHKSEYAHFRKFDLGEENFKALVLAQYLQOCPEFDHVLYNEVTEFAKTCVADSEAE 60
QY	361 CAAADPHECYAKVFDKPKLYERPKVONLQKONCFLPELGEYKFTONALVRYTKVPOYST 420	Db	1 DAHKSEYAHFRKFDLGEENFKALVLAQYLQOCPEFDHVLYNEVTEFAKTCVADSEAE 60
Db	361 CAAADPHECYAKVFDKPKLYERPKVONLQKONCFLPELGEYKFTONALVRYTKVPOYST 420	QY	61 NCDKSLTLEFDKLTQVLRLETVGENADCCAKQPERNECELOHKDNPNPRLVPEV 120
QY	421 PTLYVEYRNLGKVGSKCCKHPEAKRKPACAEYLSTYLNOLCVLHEKTPVSDRVKCCTES 480	Db	61 NCDKSLTLEFDKLTQVLRLETVGENADCCAKQPERNECELOHKDNPNPRLVPEV 120
Db	421 PTLYVEYRNLGKVGSKCCKHPEAKRKPACAEYLSTYLNOLCVLHEKTPVSDRVKCCTES 480	QY	121 DYMCTAHDNEETFKLTYETARRHPPYTAPELLFFAKRYKAFTCCQADRACLLP 180
QY	481 LYNRPCFSALEDTVTPKFEKAETPFTHADICLSEKEROQIKKQTALEVLYKPKRAT 540	Db	121 DYMCTAHDNEETFKLTYETARRHPPYTAPELLFFAKRYKAFTCCQADRACLLP 180
Db	481 LYNRPCFSALEDTVTPKFEKAETPFTHADICLSEKEROQIKKQTALEVLYKPKRAT 540	QY	181 KLDLRLDEKASSAKQURKCAASLQKFGERAKVARYARLQSOPKKAFAEYSKLVTDLK 240
QY	541 KEQLKAVMDDEAFTVEKCCKADDKETCFAEFGKKLVAAASQAAALGL 585	Db	181 KLDLRLDEKASSAKQURKCAASLQKFGERAKVARYARLQSOPKKAFAEYSKLVTDLK 240
Db	541 KEQLKAVMDDEAFTVEKCCKADDKETCFAEFGKKLVAAASQAAALGL 585	QY	241 VHTECCHGDLLECADDRADLAKYICENODSSKLKECEKPLLEKHCIAEVENDEPA 300
RESULT 2		Db	241 VHTECCHGDLLECADDRADLAKYICENODSSKLKECEKPLLEKHCIAEVENDEPA 300
AAR05318		QY	301 DLPSLAADFVESDKWNKAAXDVLGMFLYETARRHEDYSYVLLRLAKTYETTLER 360
XX	standard; protein; 585 AA.	Db	301 DLPSLAADFVESDKWNKAAXDVLGMFLYETARRHEDYSYVLLRLAKTYETTLER 360
AC	AAR05318;	QY	361 CAAADPHECYAKVFDKPKLYERPKVONLQKONCFLPELGEYKFTONALVRYTKVPOYST 420
XX	08-OCT-1990 (first entry)	Db	361 CAAADPHECYAKVFDKPKLYERPKVONLQKONCFLPELGEYKFTONALVRYTKVPOYST 420
DE	Human serum albumin gene product.	QY	421 PTLYVEYRNLGKVGSKCCKHPEAKRKPACAEYLSTYLNOLCVLHEKTPVSDRVKCCTES 480
XX	Human serum albumin; HSA-A; yeast; ds.	Db	421 PTLYVEYRNLGKVGSKCCKHPEAKRKPACAEYLSTYLNOLCVLHEKTPVSDRVKCCTES 480
OS	Homo sapiens.	QY	481 LYNRPCFSALEDTVTPKFEKAETPFTHADICLSEKEROQIKKQTALEVLYKPKRAT 540
XX	JP02117384-A.	Db	481 LYNRPCFSALEDTVTPKFEKAETPFTHADICLSEKEROQIKKQTALEVLYKPKRAT 540
PN		QY	541 KEQLKAVMDDEAFTVEKCCKADDKETCFAEFGKKLVAAASQAAALGL 585
XX		Db	541 KEQLKAVMDDEAFTVEKCCKADDKETCFAEFGKKLVAAASQAAALGL 585
AC	AAR08457;	RESULT 3	
		AAR08457	
		ID AAR08457	standard; Protein; 585 AA.
		XX	
		AC AAR08457;	

XX 25-MAR-2003 (updated)
 DT 16-APR-1991 (first entry)
 XX Human serum albumin.
 DE Human serum albumin.
 XX HSA; folding; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Region 123..303
 FT /label= A
 FT Region 1..303
 FT /label= B
 FT Region 123..585
 FT /label= C
 XX PN JP0222079-A.
 PD 10-SEP-1990.
 XX 25-AUG-1989; 89JP-0217540.
 PF 25-AUG-1989; 89JP-0217540.
 PR 25-AUG-1989; 89JP-0217540.
 XX PA (TOKU) TONEN CORP.
 XX WPI; 1990-317325/42.
 DR N-PSDB; AAQ06099.
 XX PT New human serum albumin fragments - used to bond medicines and for
 PT stable folding of protein(s).
 XX PS Claim 1; Fig 8; 24pp; Japanese.
 XX CC Fragments A-C of HSA are expressed as fusion proteins with the
 CC signal peptide of E. coli alkaline phosphatase. The fragments are
 CC selected for their specific properties. The C-terminal truncated
 CC fragment, B, does not bind long-chain fatty acids but does bind to
 CC various medicines at the central region. The N-terminal truncated
 CC fragment, C, has good stability in protein folding. The central
 CC segment, A, has characteristics of both B and C.
 CC See also AAQ06098.
 CC Updated on 25-MAR-2003 to correct PR field;
 CC Updated on 25-MAR-2003 to correct PR field;
 CC Updated on 25-MAR-2003 to correct PR field.)
 XX SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DB 11; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 DANKSEYAHREKDGLGENEATVAVLIAQYLQQCPEDHYKLYNEFEPATCVADESSE 60
 DB 1 DANKSEYAHREKDGLGENEATVAVLIAQYLQQCPEDHYKLYNEFEPATCVADESSE 60
 DB 61 NCDKSLTHLFGDKLCTVATLRETYGENADCCAKQPERNECFQHDDNPNLPRVPEY 120
 DB 61 NCDKSLTHLFGDKLCTVATLRETYGENADCCAKQPERNECFQHDDNPNLPRVPEY 120
 QY 1 DVMCTAHDNEETFLKYLKLYEIAARRHPPFYAPELLFAKEYKAATTECQADKAACCLP 180
 QY 1 DVMCTAHDNEETFLKYLKLYEIAARRHPPFYAPELLFAKEYKAATTECQADKAACCLP 180
 DB 121 KLDLRLDGKASSAKRKLQASLQEGRAFKAWAYARSQRPKAEPFAVSKLYTDLK 240
 QY 121 KLDLRLDGKASSAKRKLQASLQEGRAFKAWAYARSQRPKAEPFAVSKLYTDLK 240
 DB 121 VHTBCHGDLICADDRADLAKTCENODISSKKECCPKLIEKSHCIAEVENDMPA 300
 QY 241 VHTBCHGDLICADDRADLAKTCENODISSKKECCPKLIEKSHCIAEVENDMPA 300
 DB 241 VHTBCHGDLICADDRADLAKTCENODISSKKECCPKLIEKSHCIAEVENDMPA 300

QY 301 DLPSLAADEFVESKDVCKNTAYEAKDVFLGMLFLYVEYARRHFDYSVYLLRALKYETTLEKC 360
 DB 301 DLPSLAADEFVESKDVCKNTAYEAKDVFLGMLFLYVEYARRHFDYSVYLLRALKYETTLEKC 360
 QY 361 CAAADPHCAYAKVDEFKPKLVEFQNLKQNLCKFOLGKFKONALLVRYTAKVQVST 420
 DB 361 CAAADPHCAYAKVDEFKPKLVEFQNLKQNLCKFOLGKFKONALLVRYTAKVQVST 420
 QY 421 PTLYEVSNRLGKGSCKCKHPEAKRMPKAEDYLISVVLNOLCVLHEKTPVSDRVTKCCTES 480
 DB 421 PTLYEVSNRLGKGSCKCKHPEAKRMPKAEDYLISVVLNOLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LYNRRPCSALEYDEVYVPEKENAETFPHADICLTSERQRQKQTLALVELVKKHPKAT 540
 DB 481 LYNRRPCSALEYDEVYVPEKENAETFPHADICLTSERQRQKQTLALVELVKKHPKAT 540
 QY 541 KEQLKAVMDDEAFAVFKCCADDEKETCPAEEGKKLYAASQALGL 585
 DB 541 KEQLKAVMDDEAFAVFKCCADDEKETCPAEEGKKLYAASQALGL 585

RESULT 4
 AAR80301
 ID AAR80301 standard; Protein; 585 AA.
 XX
 AC AAR80301;
 AC AAR80301;
 XX DT 25-MAR-2003 (updated)
 DT 17-JAN-1996 (first entry)
 XX DE Human serum albumin.
 XX KW Serum albumin; HSA; aspartyl protease-3; Yap3p;
 KW Saccharomyces cerevisiae.
 XX Homo sapiens.
 XX OS Homo sapiens.
 XX PN W09523857-A1.
 XX PD 08-SEP-1995.
 XX PF 01-MAR-1995; 95W0-GB00434.
 XX PR 05-MAR-1994; 94GB-0004270.
 XX PA (DELL) DELTA BIOTECHNOLOGY LTD.
 XX PI Kerrwilliams SM, Gilbert SC;
 XX DR WPI; 1995-320572/41.
 DR N-PSDB; AAQ98895.
 XX PT Yeast with reduced levels of aspartyl protease 3 proteolytic
 PT activity - used to secrete human albumin without prodn. of the 45
 KD fragment
 XX PS Example 1; Page 26-28; 50pp; English.
 XX CC The cDNA given in AAQ98895, which encodes HSA (AAR80301), was subjected
 CC to site-directed mutagenesis to investigate the role of
 CC endoproteases in the generation of a 45 kDa albumin fragment obtd.
 CC when the cDNA is expressed in S. cerevisiae. Mutations were; R410A;
 CC I407A, L408V, V409A; and R410A, K413Q, K414Q. The latter set of
 CC mutations, specifically, improved stability of HSA to yeast Yap3p.
 CC (DELL) DELTA BIOTECHNOLOGY LTD.
 (DELL) DELTA BIOTECHNOLOGY LTD.
 XX SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 16; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255; Score 3103; DB 16;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Length 585;
 DB 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/note= "optionally acetylated, and claimed under claim 56"

FT		361 CAAADPHECYAKYDFKPLVEFQNLKQNCLEFQOLGEYKFONALLYRTKKVQVST 420
FT	XX	421 PTLYVPSRLGKVGSCKKPEAKRMPQAEDTLYVNLQOLCILHEKTVPSDLYVTRCTES 480
PN	XX	421 PTLYVPSRLGKVGSCKKPEAKRMPQAEDTLYVNLQOLCILHEKTVPSDLYVTRCTES 480
WO200020840-A1.		
XX		
XX		
PD	13-APR-2000.	
XX		
XX	01-OCT-1999;	99W0-US22905.
PF	02-OCT-1998;	98US-0102738.
XX	02-OCT-1998;	98US-0165581.
PR	02-OCT-1998;	98US-0165926.
PR	11-JAN-1999;	99US-0115382.
XX		
PA	(ISCH-) ISCHEMIA TECHNOLOGIES INC.	
XX		
PI	Bar-Or D, Lau E, Winkler JV;	
DR	XX	
XX	2000-303843/26.	
PT		New method for the continuous detection of ischemic states comprises
PT		detecting and quantifying the existence of an alteration of the serum
PT		protein albumin -
XX		
PS	Disclosure; Page 97-100; 105pp; English.	
XX		
CC		The present sequence represents human albumin protein. The specification
CC		describes a method for the continuous detection of ischemic states. The
CC		method comprises detecting and quantifying the existence of an alteration
CC		of the serum protein albumin. The method comprises contacting a
CC		biological sample containing albumin from the patient with an excess
CC		quantity of a metal ion salt, where the metal ion binds to the N-terminus
CC		of naturally occurring human albumin, to form a mixture containing bound
CC		metal ions and unbound metal ions, and then determining the amount of
CC		metal ions bound to the albumin N-terminus. The amount of bound metal
CC		ions is correlated to a known value to determine the occurrence or
CC		non-occurrence of an ischemic event. The methods are useful for detection
CC		of ischemic states. The methods are also useful for distinguishing
CC		perioperative ischemia from ischemia caused by, amongst other things,
CC		myocardial infarctions and progressive coronary artery disease.
XX		
SQ	Sequence 585 AA;	
	Query Match 100.0%; Score 3103; DB 21; Length 585;	
	Best Local Similarity 100.0%; Pred. No. 9-5e-255;	
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	1 DAHKSEVAHFKDQGEENFKALVIAFAQYQLOQCPFFEDHYKLVNTEFAKTCVADESAE 60	
	1 DAHKSEVAHFKDQGEENFKALVIAFAQYQLOQCPFFEDHYKLVNTEFAKTCVADESAE 60	
Qy	61 NDKSHHTLFGDKLCTATLRTETGEMADCAKEPERNETFLQKDDDPNLPLRTPEV 120	
Db	61 NDKSHHTLFGDKLCTATLRTETGEMADCAKEPERNETFLQKDDDPNLPLRTPEV 120	
Qy	121 DYNCTAFAHNEETFLKLYTEAHRHPTYAPLLEFAKRYKAATTECQQAADKAACLLP 180	
Db	121 DYNCTAFAHNEETFLKLYTEAHRHPTYAPLLEFAKRYKAATTECQQAADKAACLLP 180	
Qy	121 DYNCTAFAHNEETFLKLYTEAHRHPTYAPLLEFAKRYKAATTECQQAADKAACLLP 180	
Db	121 DYNCTAFAHNEETFLKLYTEAHRHPTYAPLLEFAKRYKAATTECQQAADKAACLLP 180	
Qy	181 KLDDELDEGKASSAKORLKCSLQKGERAKFAWAVARLSQRFPAEFAEYKLVTDLTK 240	
Db	181 KLDDELDEGKASSAKORLKCSLQKGERAKFAWAVARLSQRFPAEFAEYKLVTDLTK 240	
Qy	241 VHPTECCHGDLLECADDRADLAKYICENQDQSSKKECERPLKSHCIAEVENDMPA 300	
Db	241 VHPTECCHGDLLECADDRADLAKYICENQDQSSKKECERPLKSHCIAEVENDMPA 300	
Qy	301 DPLSLADFYESQDKYCNKAYDKVPLGFLYETARHEDPSVVLRLAKTYETTLK 360	
Db	301 DPLSLADFYESQDKYCNKAYDKVPLGFLYETARHEDPSVVLRLAKTYETTLK 360	
Qy	361 CAAADPHECYAKYDFKPLVEFQNLKQNCLEFQOLGEYKFONALLYRTKKVQVST 420	
Db	361 CAAADPHECYAKYDFKPLVEFQNLKQNCLEFQOLGEYKFONALLYRTKKVQVST 420	

RESULT 7
AAY83946
ID AAY83946 standard; Protein; 585 AA.
XX
AC AAY83946;
XX
PT 28-JUL-2000 (first entry)
XX
DE Yeast codon-biased recombinant human serum albumin protein.
XX
KW Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
overlapping Oligonucleotide; expression vector.
XX
KW KW
XX
PN CN1239103-A.
XX
PD 22-DEC-1999.
XX
PR 17-JUN-1998; 98CN-0102506.
XX
PR 17-JUN-1998; 98CN-0102506.
XX
PA (HAIJ-) HALJI BIOENGINEERING CO LTD.
XX
PI Li S, Lu D;
XX
DR WPE; 2000-351198/31.
DR N-PSDB; AAY10091.
XX
PT Process for preparing recombinant human serum albumin - which comprises
PT yeast biased sex codons
XX
PS Disclosure; Fig 1; 44pp; Chinese.
XX
CC The method of recombinantly producing human serum
CC albumin (HSA) in yeast by altering the coding sequence of HSA to
CC comprise a yeast codon bias. The complete HSA gene (AA10091) was
CC generated as three synthetic fragments (AA10092-10094) joined by
CC recombinant DNA technology. Each HSA fragment was synthesised from
CC overlapping Oligonucleotide fragments that were extended. This sequence
CC represents the complete sequence of the HSA encoded by the human gene
CC with a yeast codon bias. The invention also covers a recombinant
CC expression vector, yeast host cells carrying the recombinant expression
vector and the process for producing human serum albumin in the yeast
host cell, especially in secretory mode.
XX
SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 21; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.5e-255;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHFKDQGEENFKALVIAFAQYQLOQCPFFEDHYKLVNTEFAKTCVADESAE 60
Db 1 DAHKSEVAHFKDQGEENFKALVIAFAQYQLOQCPFFEDHYKLVNTEFAKTCVADESAE 60

QY 61 NCDKSILHTLPGDKLCTVATLRETYGENADCCAQKPERNECFLQHKDDNPNLPLVREY 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 NCDKSILHTLPGDKLCTVATLRETYGENADCCAQKPERNECFLQHKDDNPNLPLVREY 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 121 DYCATAFDNEETFKKLYELARRHPPYTAPELLFKRYKRAFTCCQADKACLLP 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 DYCATAFDNEETFKKLYELARRHPPYTAPELLFKRYKRAFTCCQADKACLLP 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 181 KLDLRLDEGRASSAKORLKCASTQKGERAKAWARLISQRFPKAFAEYSKLVTDLK 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 KLDLRLDEGRASSAKORLKCASTQKGERAKAWARLISQRFPKAFAEYSKLVTDLK 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 241 VHTECCGGDLECADDRADLAKYICHENODSTSSKLUKECEKPLLESHCTADEVENDMPA 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 VHTECCGGDLECADDRADLAKYICHENODSTSSKLUKECEKPLLESHCTADEVENDMPA 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 301 DLFPSLAADFVESKYCKNFAEKADVFLGMELYEVYARRHEDYSVVLRLAKTYETTLKC 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 DLFPSLAADFVESKYCKNFAEKADVFLGMELYEVYARRHEDYSVVLRLAKTYETTLKC 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 361 CAAADPHECYAKVFEDEKFKLVEPQONIKQNCELFQLEGEYKFQNALVVRPTKVPQYST 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 CAAADPHECYAKVFEDEKFKLVEPQONIKQNCELFQLEGEYKFQNALVVRPTKVPQYST 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 421 PFLVYEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSVYLNOLCVLHEKTPVSDRVTKCCES 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 PFLVYEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSVYLNOLCVLHEKTPVSDRVTKCCES 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 481 LYNRPGCSALEVDTYYPKEFNAETTFFHADICLSEKERQTKKQALVLYKHKPKAT 540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 LYNRPGCSALEVDTYYPKEFNAETTFFHADICLSEKERQTKKQALVLYKHKPKAT 540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 541 KEOQKAVMDPAAFEFKCCKADDEKTFEAERGKKLYVAASQALGL 585
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 541 KEOQKAVMDPAAFEFKCCKADDEKTFEAERGKKLYVAASQALGL 585
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
 ABBT9006
 ID ABBT9006 standard; Protein: 585 AA.
 XX
 AC ABBT9006;
 XX
 DT 01-AUG-2002 (first entry)
 XX
 DE Human mature albumin protein SEQ ID NO:18.
 XX
 KW Human; growth hormone; hGH; albumin; human serum albumin; HSA;
 KW anidiabetic; antidiabetic; antihematuric; anorectic; immunosuppressive;
 KW non-Hodgkin's lymphoma; psoriatic; cancer;
 KW type I diabetes mellitus; transplant rejection; psoriasis;
 KW
 OS Homo sapiens.
 XX
 FH Key
 FT Domain Location/Qualifiers
 FT 1..194
 FT /label= 1
 FT Domain 1..105
 FT /label= subdomain
 FT Disulfide-bond 53..62
 FT Disulfide-bond 75..91
 FT Disulfide-bond 90..101
 FT Region 106..119
 FT /note= "flexible inter-subdomain linker region"
 FT Domain 120..194
 FT Disulfide-bond 124..169
 FT Disulfide-bond 168..177
 FT Domain 195..387
 FT /label= 2
 FT Domain 195..291
 FT /label= subdomain

FT Disulfide-bond 245..253
 FT Disulfide-bond 265..279
 FT Region 278..315
 FT /note= "flexible inter-subdomain linker region"
 FT Domain 316..387
 FT /label= subdomain
 FT Disulfide-bond 360..369
 FT Domain 388..585
 FT /label= subdomain
 FT Domain 388..491
 FT /label= 3
 FT Disulfide-bond 437..448
 FT Disulfide-bond 461..477
 FT Disulfide-bond 476..487
 FT Region 492..511
 FT /note= "flexible inter-subdomain linker region"
 FT Domain 512..585
 FT /label= subdomain
 FT Disulfide-bond 514..559
 FT Disulfide-bond 558..567
 XX
 PN WO20179442-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US11850.
 XX
 PR 12-APR-2000; 2000US-229358P.
 PR 25-APR-2000; 2000US-199384P.
 PR 21-DEC-2000; 2000US-236931P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Heseltine WA;
 XX
 DR WPI; 2001-611723/70.
 XX
 PT N-PSDB; ASN87288.
 XX
 PT New albumin fusion proteins, useful for treating diseases and disorders
 XX such as cancer, comprise therapeutic protein fused to albumin -
 XX
 PS Claim 1; Fig 11; 413pp; English.
 XX
 DR WPI; 2001-611723/70.
 XX
 PT New albumin fusion proteins, useful for treating diseases and disorders
 XX such as cancer, comprise therapeutic protein fused to albumin -
 XX
 PS Claim 1; Fig 11; 413pp; English.
 XX
 CC the present invention describes an albumin fusion protein (I) comprising
 CC a therapeutic protein: X and (a fragment or variant of) albumin
 CC comprising a the fully functional sequence in ABBT9006 of 585 amino acids,
 CC (where the fragment or variant has albumin or therapeutic protein: X
 CC activity). (I) can have cytostatic, anorectic, immunosuppressive,
 CC antidiabetic, antirheumatic, antiarthritic, psoriatic, immunosuppressive,
 CC albumin fusion proteins are stabilised therapeutic proteins e.g.
 CC antibodies to C5, C242 and C60 useful for treating various diseases
 CC and disorders such as non-Hodgkin's lymphoma, cancer, obesity,
 CC transplant rejection, type I diabetes mellitus, rheumatoid arthritis
 CC and psoriasis. Fusing albumin to therapeutic proteins stabilises the
 CC therapeutic protein, extends the shelf life and retains the in vitro or
 CC in vivo biological activity. It also reduces the need to formulate
 CC protein solutions with large excesses of carrier proteins to prevent
 CC loss of therapeutic proteins due to factors such as binding to the
 CC container. The fusion proteins are easily dispensed with a simple
 CC formulation requiring minimal post storage manipulation. The fusion of
 CC therapeutic proteins to albumin confers stability in aqueous or other
 CC solution. The present sequence represents the mature human albumin (HA)
 CC protein which is used in the exemplification of the present invention.
 XX
 SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FT

Db 121 DVACTAHDNEETFLKKVYETARRHYFVAPELLFAFRYKAFTCCQADKAACILP 180
 QY 181 KLDLDRDGKASSAQRKLCASQKGERAKAWARYSQRPKAFAEVSKLYVIDLTK 240
 Db 181 KLDLDRDGKASSAQRKLCASQKGERAKAWARYSQRPKAFAEVSKLYVIDLTK 240
 QY 241 VHTECGHDLLCADDRADLAKTYCENODTSKSKKECEKPLLEKSHCIAEVENDMA 300
 Db 241 VHTECGHDLLCADDRADLAKTYCENODTSKSKKECEKPLLEKSHCIAEVENDMA 300
 QY 301 DLPSLAADFVESKDVKYNAEADFLGMFLYETARRHFDYSVLLRLAKTYETLERC 360
 Db 301 DLPSLAADFVESKDVKYNAEADFLGMFLYETARRHFDYSVLLRLAKTYETLERC 360
 QY 361 CAADPHECYAKVFEDEKFPLVEPQNLKQNLKQNLKQNLKQNLKQNLKQVST 420
 Db 361 CAADPHECYAKVFEDEKFPLVEPQNLKQNLKQNLKQNLKQNLKQNLKQVST 420
 QY 421 PTLYEVSRLGKVGSKCKXHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRTKCCTES 480
 Db 421 PTLYEVSRLGKVGSKCKXHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRTKCCTES 480
 QY 481 LYNRPCFSALEVEDTYVKEPKNAEPTTFHADICLSEKERQIKKOPALVELVKPKAT 540
 Db 481 LYNRPCFSALEVEDTYVKEPKNAEPTTFHADICLSEKERQIKKOPALVELVKPKAT 540
 QY 541 KEQIKAVMDPDAAFTEKCKKADDKETCEAEGKKLVAAQOALGL 585
 Db 541 KEQIKAVMDPDAAFTEKCKKADDKETCEAEGKKLVAAQOALGL 585

RESULT 10

ID AAM52567 standard; Protein: 585 AA.

AC AAM52567;

DT 05-FEB-2002 (first entry)

XX Mature human serum albumin.

XX Human; serum albumin; HA; antiinflammatory; immunosuppressive; cardiotonic; nootropic; neuroprotective; gene therapy; immune therapy; wound healing; hyperproliferative disorder; renal disorder; cardiovascular disorder; respiratory disorder; neurological disease; endocrine disorder; reproductive system disorder; infectious disease; gastrointestinal disorder.
 XX Homo sapiens.

OS Homo sapiens.

XX

PN W0200179444-A2.

XX

DR 25-OCT-2001.

XX

PF 12-APR-2001; 2001WO-US12013.

XX

PR 12-APR-2000; 2000US-229458P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256331P.

XX (DNA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Haseltine WA;

XX

DR WPI: 2001-616755/71.

DR N-PSDB; ABA03057.

XX Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders -

XX

PA Human albumin (HA).

PS Claim 1; Fig 15; 606pp; English.
 XX The present invention relates to albumin fusion proteins, which comprise a therapeutic protein and albumin. The present sequence is the protein sequence for mature human serum albumin (HA), which was used to generate the fusion proteins of the present invention. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases/disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. glomerulonephritis, cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. Alzheimer's disease), endocrine disorders (e.g. phaeochromoma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. irritable bowel syndrome) and wound healing.

Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-25;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFKDGLKLTATLRLTYGMDACAKOEPENECLQHKDDPFLNPLVRE 120
 Db 1 DAHKSEVAHFKDGLKLTATLRLTYGMDACAKOEPENECLQHKDDPFLNPLVRE 120
 QY 61 NCDKSHLTFGDKLTATLRLTYGMDACAKOEPENECLQHKDDPFLNPLVRE 120
 Db 61 NCDKSHLTFGDKLTATLRLTYGMDACAKOEPENECLQHKDDPFLNPLVRE 120

QY 121 DYMCTAFHNEEFKLKYLYETARRHPPYFAPELLEFAKRYKAFTCCQADKAACILP 180
 Db 121 DYMCTAFHNEEFKLKYLYETARRHPPYFAPELLEFAKRYKAFTCCQADKAACILP 180

QY 181 KLDLDRDGKASSAKQRKUCASLQKFGRAFKAWAVALSQRFPKAFEVSKLVTDLRK 240
 Db 181 KLDLDRDGKASSAKQRKUCASLQKFGRAFKAWAVALSQRFPKAFEVSKLVTDLRK 240

QY 241 VHTECGHDLLCADDRADLAKYICENODTSKSKKECEKPLLEKSHCIAEVENDMA 300
 Db 241 VHTECGHDLLCADDRADLAKYICENODTSKSKKECEKPLLEKSHCIAEVENDMA 300

QY 301 DIPSLADEFVSKDVKYNAFADKYLGMFLYETARRHFDYSVLLRLAKTYETTLEK 360
 Db 301 DIPSLADEFVSKDVKYNAFADKYLGMFLYETARRHFDYSVLLRLAKTYETTLEK 360

QY 361 CAAADEHECYAKVDEFKPLVPEPONLKLONCELEQIGETKFQNALLRTYKPVQST 420
 Db 361 CAAADEHECYAKVDEFKPLVPEPONLKLONCELEQIGETKFQNALLRTYKPVQST 420

QY 421 PTLYEVSRLGKVGSKCKXHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRTKCCTES 480
 Db 421 PTLYEVSRLGKVGSKCKXHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRTKCCTES 480

QY 481 LYNRPCFSALEVEDTYVKEPKNAEPTTFHADICLSEKERQIKKOPALVELVKPKAT 540
 Db 481 LYNRPCFSALEVEDTYVKEPKNAEPTTFHADICLSEKERQIKKOPALVELVKPKAT 540

QY 541 KEQIKAVMDPDAAFTEKCKKADDKETCEAEGKKLVAAQOALGL 585
 Db 541 KEQIKAVMDPDAAFTEKCKKADDKETCEAEGKKLVAAQOALGL 585

RESULT 11
 AAE13129
 XX
 AC
 XX
 DT 28-JAN-2002 (first entry)
 DE Human albumin (HA).

XX Human; albumin; HA; fusion protein; therapeutic protein; vulnerable;
 KW immune system disorder; transplant rejection; blood related disorder;
 KW myocardial infarction; hyperproliferative disorder; glomerulonephritis;
 KW childhood acute myeloid leukaemia; cardiovascular disorder; arrhythmia;
 KW respiratory disorder; gene therapy; non-allergic rhinitis; nootropic;
 KW neurological disease; Alzheimer's disease; reproductive system disorder;
 KW endocrine disorder; phaeochromocytoma; infectious disease; antiarthritis;
 KW measles; gastrointestinal disorder; irritable bowel syndrome; syphilis;
 KW wound healing; antiinflammatory; immunosuppressive; neuroprotective;
 KW cardiant; cytostatic; anti-leukaemic; antirheumatic; antimicrobial;
 KW renal disorder.
 XX OS Homo sapiens.

Location/Qualifiers

XX FH Key
 FT Domain 54..61
 FT Domain /label= Loop_I
 FT Domain 76..89
 FT Domain /label= Loop_II
 FT Domain 92..100
 FT Domain /label= Loop_III
 FT Domain 170..176
 FT Domain /label= Loop_IV
 FT Domain 247..252
 FT Domain /label= Loop_V
 FT Domain 266..277
 FT Domain 280..288
 FT Domain /label= Loop_VI
 FT Domain 362..368
 FT Domain /label= Loop_VII
 FT Domain 439..447
 FT Domain /label= Loop_VIII
 FT Domain 461..475
 FT Domain /label= Loop_X
 FT Domain 478..486
 FT Domain /label= Loop_XI
 FT Domain 560..566
 FT Domain /label= Loop_XII
 XX PN WO2001179443-A2.
 XX PD 25-OCT-2001.
 XX PP 12-APR-2001; 2001WO-US11924.

XX DR WPI: 2001-616754/71.

DR N-PSDB; AAD21638.

XX PT Albumin fusion proteins comprising a therapeutic protein and albumin,
 PT useful in the treating immune system disorders (e.g. transplant
 PT rejection), blood related disorders (e.g. myocardial infarction) and
 PT hyperproliferative disorders -

XX PA (HUMAN) HUMAN GENOME SCI INC.

P1 Rosen CA, Haseltine WA;

XX DR WPI: 2001-616754/71.

DR N-PSDB; AAD21638.

XX PT

PT The invention relates to albumin fusion proteins comprising therapeutic
 CC protein and human albumin (HA). Therapeutic protein fused to albumin
 CC have an extended shelf-life. The albumin fusion proteins are useful in
 CC the treatment, prevention, diagnosis and/or detection of diseases,
 CC disorders such as immune system disorders (e.g. transplant rejection),
 CC blood related disorders (e.g. myocardial infarction), hyperproliferative
 CC disorders (e.g. childhood acute myeloid leukaemia), renal disorders
 CC (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias),

CC respiratory disorders (e.g. non-allergic rhinitis), neurological
 CC diseases (e.g. Alzheimer's disease), endocrine disorders (e.g.
 CC pheochromocytoma), reproductive system disorders (e.g. syphilis),
 CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
 CC irritable bowel syndrome) and wound healing. Nucleic acids encoding
 CC albumin fusion protein is used in gene therapy. The present sequence
 CC is human albumin (HA) protein.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
 Best Local Similarity 100.0%; Prd. No. 9.5e-25; Indels 0; Gaps 0;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEYAHREKFDLGEENENKALVLIATAQYIQQCPEDKVLYNEVTEFAKTCVADESE 60
 DB 1 DAHKSEYAHREKFDLGEENENKALVLIATAQYIQQCPEDKVLYNEVTEFAKTCVADESE 60
 QY 61 NCDKSLHTLFGDKLCLVATLREPVYGENADCGAKQSPERNECFLQHKDQNPPLPVRPV 120
 DB 61 NCDKSLHTLFGDKLCLVATLREPVYGENADCGAKQSPERNECFLQHKDQNPPLPVRPV 120
 QY 121 DVMCTAHDNEETFLKYLTEIARRHPPYTAPELIFFKRYKAFTFCQADKAACLLP 180
 DB 121 DVMCTAHDNEETFLKYLTEIARRHPPYTAPELIFFKRYKAFTFCQADKAACLLP 180
 QY 181 KLDLERDGGASSAKRLLKCASTOKGEPAFKAWAYLSQLPKEAFYSKLVTDIJK 240
 DB 181 KLDLERDGGASSAKRLLKCASTOKGEPAFKAWAYLSQLPKEAFYSKLVTDIJK 240
 QY 241 VHTECGDPLLCADRADIAKIZCENODLSSSKKECCKPLKESCIAYEVDENDPA 300
 DB 241 VHTECGDPLLCADRADIAKIZCENODLSSSKKECCKPLKESCIAYEVDENDPA 300
 QY 361 CAAADPHCYAKYDEFKPLVEEPONL1KONCEFLFOLGYTKFQNALLYRVTKYPQVST 420
 DB 361 CAAADPHCYAKYDEFKPLVEEPONL1KONCEFLFOLGYTKFQNALLYRVTKYPQVST 420
 QY 421 PTLVEVSRNLGKGSKCKHPKPEAKMPAEDYLSVYVNLQCVLHEKTPVSDRVTKCOTES 480
 DB 421 PTLVEVSRNLGKGSKCKHPKPEAKMPAEDYLSVYVNLQCVLHEKTPVSDRVTKCOTES 480
 QY 481 LYNRPCSALEYDTPYKEFNAETFFHADICLTSLEKERTQKOTALVLYHKPKAT 540
 DB 481 LYNRPCSALEYDTPYKEFNAETFFHADICLTSLEKERTQKOTALVLYHKPKAT 540
 QY 541 KEQLKAVMDDFAAFKVCKCADDKETCPAEGKKLVASQALGL 585
 DB 541 KEQLKAVMDDFAAFKVCKCADDKETCPAEGKKLVASQALGL 585

RESULT 1.2
 AAEE12403 standard; Protein: 585 AA.

XX ID AAEE12403;
 XX AC AAEE12403;
 XX DT 18-DEC-2001 (first entry)
 XX DE Human albumin (HA).

XX KW Human; albumin; HA; immune system disorder; transplant rejection;
 KW blood related disorder; myocardial infarction; glomerulonephritis;
 KW hyperproliferative disorder; childhood acute myeloid leukaemia;
 KW real cell carcinoma; cardiovascular disorder; pulmonary melanoma;
 KW arrhythmia; respiratory disorder; non-allergic rhinitis; antileukaemic;
 KW neurological disease; Alzheimer's disease; endocrine disorder; measles;
 KW phaeochromocytoma; reproductive system disorder; neuroprotective; syphilis;
 KW infectious disease; gastrointestinal disorder; wound healing; nootropic;

XX WPI; 2001-540371/60.
 DR N-PSDB; A011488.
 XX Measuring human cell proliferation, useful in drug screening to determine the potential for inhibiting cancer cell proliferation and for evaluating biopsied tumors, comprises employing albumin-derived peptide
 XX PS Claim 1; Fig 1; 20pp; English.
 XX The invention related to a method for testing cancer cells. The method is useful for measuring human cancer cell proliferation, particularly for determining the potential for inhibiting cancer cells proliferation using albumin-derived peptides. The invention is also useful for drug screening assays, as well as for evaluating biopsied tumours. The present sequence is human serum albumin (HSA) related to the invention.
 XX SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DB 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 385; Conservative 0; Mismatches 0; Gaps 0;
 Db 1 DAHKSYVAHREFKDGEENFKALVYIAFAQYIQQCPEEDHVKLYNEVTEFAKTCVADESAE 60
 1 DAHKSYVAHREFKDGEENFKALVYIAFAQYIQQCPEEDHVKLYNEVTEFAKTCVADESAE 60
 Qy 61 NCDDKSUHTLEGDKLCTVATLRTYGMADCAKQDPERNECFLQHDDNPNLPLVPEV 120
 61 NCDDKSUHTLEGDKLCTVATLRTYGMADCAKQDPERNECFLQHDDNPNLPLVPEV 120
 Db 121 DYMCTAFAHDNEETFLKKYLYEARIARHPPYFAYAPELLFFKRYKAFFTECCOAADKAACLLP 180
 121 DYMCTAFAHDNEETFLKKYLYEARIARHPPYFAYAPELLFFKRYKAFFTECCOAADKAACLLP 180
 Db 181 KLDERDEGKASSAKORLKCASTQKGERAKAWAVALSORPKFAFAEVSKLYVDTLK 240
 181 KLDERDEGKASSAKORLKCASTQKGERAKAWAVALSORPKFAFAEVSKLYVDTLK 240
 Qy 241 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 300
 241 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 300
 Db 301 DLPSLADFYESKVKCKRNAYAEDVFLGMLFYEARHPPDYSVLLRLAKRTYETTLKCK 360
 301 DLPSLADFYESKVKCKRNAYAEDVFLGMLFYEARHPPDYSVLLRLAKRTYETTLKCK 360
 Qy 361 CAAADPHECYAKVDFEKFPLVPEQNLIKONCELEQIGEYKEQNLVLYTCKVQYST 420
 361 CAAADPHECYAKVDFEKFPLVPEQNLIKONCELEQIGEYKEQNLVLYTCKVQYST 420
 Db 421 PTIIVEYSRNLGKVGSKCCKHPPEAKRMPCAEDYLSVNLNQLCYLHEKTPSDRVTKCCTES 480
 421 PTIIVEYSRNLGKVGSKCCKHPPEAKRMPCAEDYLSVNLNQLCYLHEKTPSDRVTKCCTES 480
 Qy 481 LYNNRPPSALEDETYTPKEENAEPTFADICLTSERERQIKKQTALEVLYKHKPKAT 540
 481 LYNNRPPSALEDETYTPKEENAEPTFADICLTSERERQIKKQTALEVLYKHKPKAT 540
 Db 541 KEQLKAVMDDFAAVFEKCKADDKETCFAEFGKLYVAASQAAIGL 585
 541 KEQLKAVMDDFAAVFEKCKADDKETCFAEFGKLYVAASQAAIGL 585
 Db 585 AA;

RESULT 14
 ABG71291
 ID ABG71291 standard; Protein; 585 AA.
 XX AC ABG71291;
 DT 08-JAN-2003 (first entry)

DE Glycosylated protein determination associated protein.
 XX Standard substance; accuracy control substance; glycosylated protein;
 KW glycosylated albumin; fructosamine; diabetes; antidiabetic.
 XX Unidentified.
 OS XX
 PT PN JP2002243731-A.
 XX XX
 PD 28-AUG-2002.
 XX XX
 PF 21-FEB-2001; 2001JP-0045085.
 XX XX
 PR 21-FEB-2001; 2001JP-0045085.
 XX XX
 PA (KOKU-) KOKUSAI SHIYAKU KK.
 PA (YOSH-) YOSHITOMI PHARM IND KK.
 XX XX
 DR WPI; 2002-744850/81.
 XX XX
 PT A standard substance for determination of glycosylated protein including glycosylated albumin and fructosamine, used in diagnosis of diabetes -
 XX PS Disclosure; Page 4; 6pp; Japanese.
 CC The present invention relates to a new standard and accuracy control substance for determination of glycosylated protein. The invention is useful for determination of glycosylated protein in the diagnosis of diabetes. Glycosylated albumin and fructosamine provide favourable dilution linearity. The present amino acid sequence represents the glycosylated protein determination associated protein as described in the invention.
 CC
 XX SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DB 23; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DAHKSYVAHREFKDGEENFKALVYIAFAQYIQQCPEEDHVKLYNEVTEFAKTCVADESAE 60
 1 DAHKSYVAHREFKDGEENFKALVYIAFAQYIQQCPEEDHVKLYNEVTEFAKTCVADESAE 60
 Qy 1 DAHKSYVAHREFKDGEENFKALVYIAFAQYIQQCPEEDHVKLYNEVTEFAKTCVADESAE 60
 1 DAHKSYVAHREFKDGEENFKALVYIAFAQYIQQCPEEDHVKLYNEVTEFAKTCVADESAE 60
 Db 61 NCDDKSUHTLEGDKLCTVATLRTYGMADCAKQDPERNECFLQHDDNPNLPLVPEV 120
 61 NCDDKSUHTLEGDKLCTVATLRTYGMADCAKQDPERNECFLQHDDNPNLPLVPEV 120
 Qy 121 DYMCTAFAHDNEETFLKKYLYEARIARHPPYFAYAPELLFFKRYKAFFTECCOAADKAACLLP 180
 121 DYMCTAFAHDNEETFLKKYLYEARIARHPPYFAYAPELLFFKRYKAFFTECCOAADKAACLLP 180
 Db 181 KLDERDEGKASSAKORLKCASTQKGERAKAWAVALSORPKFAFAEVSKLYVDTLK 240
 181 KLDERDEGKASSAKORLKCASTQKGERAKAWAVALSORPKFAFAEVSKLYVDTLK 240
 Qy 241 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 300
 241 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 300
 Db 301 DLPSLADFYESKVKCKRNAYAEDVFLGMLFYEARHPPDYSVLLRLAKRTYETTLKCK 360
 301 DLPSLADFYESKVKCKRNAYAEDVFLGMLFYEARHPPDYSVLLRLAKRTYETTLKCK 360
 Qy 361 CAAADPHECYAKVDFEKFPLVPEQNLIKONCELEQIGEYKEQNLVLYTCKVQYST 420
 361 CAAADPHECYAKVDFEKFPLVPEQNLIKONCELEQIGEYKEQNLVLYTCKVQYST 420
 Db 420 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 300
 420 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 300
 Qy 421 DLPSAADFVEKDYCKNAYAEDVFLKLYTETPLAKYETTLEK 360
 421 DLPSAADFVEKDYCKNAYAEDVFLKLYTETPLAKYETTLEK 360
 Db 360 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 360 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 Qy 361 CAAADPHECYAKVDFEKFPLVPEQNLIKONCELEQIGEYKEQNLVLYTCKVQYST 420
 361 CAAADPHECYAKVDFEKFPLVPEQNLIKONCELEQIGEYKEQNLVLYTCKVQYST 420
 Db 420 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 420 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 Qy 421 PTIIVEYSRNLGKVGSKCCKHPPEAKRMPCAEDYLSVNLNQLCYLHEKTPSDRVTKCCTES 480
 421 PTIIVEYSRNLGKVGSKCCKHPPEAKRMPCAEDYLSVNLNQLCYLHEKTPSDRVTKCCTES 480
 Db 480 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 480 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 Qy 481 LYNNRPPSALEDETYTPKEENAEPTFADICLTSERERQIKKQTALEVLYKHKPKAT 540
 481 LYNNRPPSALEDETYTPKEENAEPTFADICLTSERERQIKKQTALEVLYKHKPKAT 540
 Db 540 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 540 VTECCHGDLLECAADDRADLAKYICENQDSSSSKKECECKPPLKEKSHCIAEVENDEPKA 360
 Qy 541 KEQLKAVMDDFAAVFEKCKADDKETCFAEFGKLYVAASQAAIGL 585
 541 KEQLKAVMDDFAAVFEKCKADDKETCFAEFGKLYVAASQAAIGL 585
 Db 585 AA;

481 LYVRRPCSALEVDDETTYKKEVAAETTEHADICLSEERQTKKTAIVELVHKPAT 540
 QY 541 KEQIKAVADDEAFTVEKCKADDEKETCFAEKGKKLVAASQAAIGL 585
 QY 541 KEQIKAVADDEAFTVEKCKADDEKETCFAEKGKKLVAASQAAIGL 585

RESULT 15
 ABG63321 standard; protein; 585 AA.
 XX ABG63321;
 AC
 XX DT 27-AUG-2002 (first entry)
 XX DE Human serum albumin (HSA) protein.
 XX KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematoopoietic disorder; neural disorder; connective disorder;
 KW cytotoxic; antiinflammatory; antiulcer; immunomodulator;
 KW immunomodulatory; anti-HIV; antidiabetic; haemostatic; nontropic;
 KW neuroprotective; autiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic;
 XX OS Homo sapiens.
 XX PN WO200117137-A1.
 XX PD 18-OCT-2001.
 XX PP 12-APR-2001; 2001WO-US11988.
 XX PR 12-APR-2000; 2000US-229358P.
 PR 21-APR-2000; 2000US-199384P.
 PR 21-DRC-2000; 2000US-256911P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Haseltine WA;
 XX DR WPI; 2002-010886/01.
 DR N-PSDB; ABK93280.
 XX PT New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein -
 XX PS Claim 1; Fig 15; 210pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or
 CC disorder that may be modulated by therapeutic protein X. The albumin
 CC extends the shelf-life of protein X, and may increase its biological
 CC in vitro/in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
 CC (e.g. diabetes), haemopoietic disorders, neural disorders
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). The present sequence represents HA
 CC (HA) protein.
 XX SQ Sequence 585 AA;

Db 1 DAHSEVAHREFDLDGEENFKALVLLAFAQYILOQCPEDHYKLYNEVTEFAKTCVADESAE 60
 QY 61 NCDSLPLFEGDLCLVATREYGMEDCCAKQEPERNECFLQHDNPNEPLVYRPEV 120
 Db 61 NCDSLPLFEGDLCLVATREYGMEDCCAKQEPERNECFLQHDNPNEPLVYRPEV 120
 QY 121 DVMCTAHDNEETFLKLYLEIARRHPPYFAYELLEFAKRYKAFAFTECCQAADKAACLLP 180
 Db 121 DVACTAHDNEETFLKLYLEIARRHPPYFAYELLEFAKRYKAFAFTECCQAADKAACLLP 180
 QY 181 KLDEIRDEGKASSAKOKLCAASLQFKGRAFKAWARYLSQSRPKAEPAEVSKLYDLM 240
 Db 181 KLDEIRDEGKASSAKOKLCAASLQFKGRAFKAWARYLSQSRPKAEPAEVSKLYDLM 240
 QY 241 VHTECCHGDLLCADRADAKYICENDSISKLKECCCKPYLEKSHCATVENDEMPA 300
 Db 241 VHTECCHGDLLCADRADAKYICENDSISKLKECCCKPYLEKSHCATVENDEMPA 300
 QY 301 DLPSLADEVESKDVCKNYAKAKVFLGAFMFLKEYARRHPPDSTVLLRALKYETTELEKC 360
 Db 301 DLPSLADEVESKDVCKNYAKAKVFLGAFMFLKEYARRHPPDSTVLLRALKYETTELEKC 360
 QY 361 CAAADPHECYAKVDEEKFPLVEEFQNLKQNCLETFOLGEKFONALYRTKVQVSP 420
 Db 361 CAAADPHECYAKVDEEKFPLVEEFQNLKQNCLETFOLGEKFONALYRTKVQVSP 420
 QY 421 PTLYEVSRNLGKYGSCKKPEAKRMPAEDYTSVVLNQCLVYEEKTPSDRVTKCCTES 480
 Db 421 PTLYEVSRNLGKYGSCKKPEAKRMPAEDYTSVVLNQCLVYEEKTPSDRVTKCCTES 480
 QY 481 LVNRPFCSALEYDENVYKPEKENETTFHADICLSEKERQIKTQTAIVELYKHKPKAT 540
 Db 481 LVNRPFCSALEYDENVYKPEKENETTFHADICLSEKERQIKTQTAIVELYKHKPKAT 540
 QY 541 KEQLKAVMDDFAAFVERCKKADDKETCFAEKGKKLYAZASQAGL 585
 Db 541 KEQLKAVMDDFAAFVERCKKADDKETCFAEKGKKLYAZASQAGL 585

Search completed: August 31, 2003, 16:38:41
 Job time : 86 secs

Query Match 100.0%; Score 3103; DB 23; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e 255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHREFDLDGEENFKALVLLAFAQYILOQCPEDHYKLYNEVTEFAKTCVADESAE 60

result	No.	Score	Query	Match	Length	DB	ID	Description
1	3103	100.0	585	1	US-08-153-799-14	Sequence 14, Appli		Sequence 14, Appli
2	3103	100.0	585	2	US-08-702-572-2	Sequence 2, Appli		Sequence 2, Appli
3	3103	100.0	585	3	US-08-769-746-2	Sequence 2, Appli		Sequence 2, Appli
4	3103	100.0	610	2	US-08-789-689-2	Sequence 2, Appli		Sequence 2, Appli
5	3103	100.0	783	1	US-08-256-938-2	Sequence 4, Appli		Sequence 4, Appli
6	3103	100.0	787	1	US-08-938-84	Sequence 16, Appli		Sequence 16, Appli
7	3103	100.0	787	1	US-08-797-689-16	Sequence 3, Appli		Sequence 3, Appli
8	3099	99.9	609	1	US-08-222-619-3	Sequence 4, Appli		Sequence 4, Appli
9	3099	99.9	609	1	US-08-133-637-4	Sequence 2, Appli		Sequence 2, Appli
10	3099	99.9	609	4	US-08-897-956A-2	Sequence 3, Appli		Sequence 3, Appli
11	3099	99.9	609	5	PCP-US95-040753	Sequence 3, Appli		Sequence 3, Appli
12	3095	99.7	978	4	US-08-897-556A-3	Sequence 1, Appli		Sequence 1, Appli
13	3093	99.7	585	1	US-08-448-196A-3	Sequence 1, Appli		Sequence 1, Appli
14	3093	99.7	585	2	US-08-984-176-1	Sequence 5, Appli		Sequence 5, Appli
15	2458.5	79.2	583	1	US-08-448-196A-5	Sequence 4, Appli		Sequence 4, Appli
16	2450.5	79.0	583	1	US-08-448-196A-4	Sequence 6, Appli		Sequence 6, Appli
17	2432.5	78.4	583	1	US-08-448-196A-6	Sequence 7, Appli		Sequence 7, Appli
18	2426	78.2	584	1	US-08-134-638-1	Sequence 1, Appli		Sequence 1, Appli
19	2389	77.0	582	1	US-08-222-519-4	Sequence 4, Appli		Sequence 4, Appli
20	1249.5	40.3	609	1	PCP-US95-040754	Sequence 2, Appli		Sequence 2, Appli
21	1249.5	40.3	609	2	US-08-377-809-2	Sequence 3, Appli		Sequence 3, Appli
22	1206.5	38.9	590	3	US-09-186-723-2	Sequence 5, Appli		Sequence 5, Appli
23	1206.5	38.9	590	4	US-08-505-012-5	Sequence 3, Appli		Sequence 3, Appli
24	1206.5	38.9	590	4	US-09-186-949A-3	Sequence 5, Appli		Sequence 5, Appli
25	1206.5	38.9	590	4	US-08-758-757-7	Sequence 8, Appli		Sequence 8, Appli
26	1206.5	38.9	590	5	PCP-US95-00996-5	Sequence 5, Appli		Sequence 5, Appli

MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 FEATURE:
 NAME/KEY: Region
 LOCATION: 369-419
 OTHER INFORMATION: /note= "Alternative C-termini of
 HSA (1-n)"
 OTHER INFORMATION:
 NAME/KEY: Region
 LOCATION: 1..585
 OTHER INFORMATION: /note= "Amino acid sequence of
 natural HSA"
 US-08-153-799-14

Query Match 100.0%; Score 3103; DB: 1; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.3e-287;
 Matches 585; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 DAHKSEVAFHKDQEENFKALVIAAQYLQQCPFEDHKVLYNEVTEFAKTCVADSE 60
 Db 1 DAHKSEVAFHKDQEENFKALVIAAQYLQQCPFEDHKVLYNEVTEFAKTCVADSE 60

Qy 61 NCDDKSLHTLFDKLCTVATLRLTYGENADCCAKQEPERNECFLQHDDNPNLPRLYRPEV 120
 Db 61 NCDDKSLHTLFDKLCTVATLRLTYGENADCCAKQEPERNECFLQHDDNPNLPRLYRPEV 120

Qy 121 DYNCTAHDNNEFTFLKKLYETARRHRYFYAPELIFFAKRYKRAFTCCQAAKACLIP 180
 Db 121 DYNCTAHDNNEFTFLKKLYETARRHRYFYAPELIFFAKRYKRAFTCCQAAKACLIP 180

Qy 181 KLDDELDEGKASSAKQRLKCASTQKGERAKWAVARLQSOPKPAFAEYSKLVTDLT 240
 Db 181 KLDDELDEGKASSAKQRLKCASTQKGERAKWAVARLQSOPKPAFAEYSKLVTDLT 240

Qy 241 VHTECCHDLLIECAADDRLAKYTCENQDSSTSSKLIKECEKPLLESHCTADEVENDPA 300
 Db 241 VHTECCHDLLIECAADDRLAKYTCENQDSSTSSKLIKECEKPLLESHCTADEVENDPA 300

Qy 301 DLPSLAADFYESKDVCKNYAEEKDVLGMFLIYEYARRHDPDSYVLLRLAKTYETTLRKC 360
 Db 301 DLPSLAADFYESKDVCKNYAEEKDVLGMFLIYEYARRHDPDSYVLLRLAKTYETTLRKC 360

Qy 361 CAAADPHECYAKVDEEFPKLYEPONLIKONCELEFOLGEKYKPNALIVRTKYPQST 420
 Db 361 CAAADPHECYAKVDEEFPKLYEPONLIKONCELEFOLGEKYKPNALIVRTKYPQST 420

Qy 421 PTLYVEYSRNLGKVGSKCKKHPKRPKAEPADYLSTVLNOLCVLHEKTPVSDRVKCCTES 480
 Db 421 PTLYVEYSRNLGKVGSKCKKHPKRPKAEPADYLSTVLNOLCVLHEKTPVSDRVKCCTES 480

Qy 481 LYNRPCFSALEVDTYYPKEFNAETFTFHADICLSEKERQIKKOTALYELVKHKPKAT 540
 Db 481 LYNRPCFSALEVDTYYPKEFNAETFTFHADICLSEKERQIKKOTALYELVKHKPKAT 540

Qy 541 KEQLKAVMDPDAAFYTFEKCKADDKETCFAPAEGKKLVAAASQAAQL 585
 Db 541 KEQLKAVMDPDAAFYTFEKCKADDKETCFAPAEGKKLVAAASQAAQL 585

RESULT 2
 US-08-702-572-2
 Sequence 2, Application US/08/702572
 Patent No. 5965386
 GENERAL INFORMATION:
 APPLICANT: Kerr-Williams, Sean M
 TITLE OF INVENTION: Test Strains and Modified Albumins
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Centeon L.L.C.
 STREET: 1020 First Avenue

Query Match 100.0%; Score 3103; DB 3; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.3e-287;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 ; Sequence 2, Application US/08769746
 ; Patent No. 6274305
 ; GENERAL INFORMATION:
 ; APPLICANT: Sonnenschein, Carlos
 ; APPLICANT: Soto, Ana M.
 ; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Medlen Carroll, LLP
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/769,746
 FILING DATE: 19-DEC-1996
 CLASSIFICATION INFORMATION:
 CLASSIFICATION NUMBER: 435
 NAME: Carroll, Peter G.
 REFERENCE/DOCKET NUMBER: MBRI-02584

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 397-8388
 TELEFAX: (415) 705-8410

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 585 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-769-746-2

Query Match 100.0%; Score 3103; DB 3; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.3e-287;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAHSEVAHFRKDGLBENFALVIAFQYQLOQCPPEHDYKLYNEVTEFAKTCVDAESE 60
 1 DAHSEVAHFRKDGLBENFALVIAFQYQLOQCPPEHDYKLYNEVTEFAKTCVDAESE 60

61 NCDSLALTFGDKLCPVATLRTYGENADCCAKOEPERNCFLOHDNPPLRVRPEY 120
 61 NCDSLALTFGDKLCPVATLRTYGENADCCAKOEPERNCFLOHDNPPLRVRPEY 120

121 DVMCTAIDNEETFLKLYTEIATRHPFYTAELFVAKTCAEADKACCLP 180
 121 DVMCTAIDNEETFLKLYTEIATRHPFYTAELFVAKTCAEADKACCLP 180

181 KIDELRDEKASSAKQRLKACASLQREGERAKAWAYARLSQRFKAEFAEYSKLYVLDLK 240
 181 KIDELRDEKASSAKQRLKACASLQREGERAKAWAYARLSQRFKAEFAEYSKLYVLDLK 240

241 VHTECCHGDLBEGADDRLAKYKENODSSKKECCPKLKSCTIAEVENEMPA 300
 241 VHTECCHGDLBEGADDRLAKYKENODSSKKECCPKLKSCTIAEVENEMPA 300

301 DPLSIAADDFVSESDVCNYAAKDVKFLGMLFLYKARRHPDSVYLLRLAKTYETFLKC 360
 301 DPLSIAADDFVSESDVCNYAAKDVKFLGMLFLYKARRHPDSVYLLRLAKTYETFLKC 360

QY 541 KEQKATADPAAVTEKCOAKADKEQFAEGKKVLAASQALGL 585
 Db 541 KEQKATADPAAVTEKCOAKADKEQFAEGKKVLAASQALGL 585
 QY 361 CAAADPHECTAKVDFKPLVEPQNLIKONCELEQGEYKQONALRYTKVPOVST 420
 Db 361 CAAADPHECTAKVDFKPLVEPQNLIKONCELEQGEYKQONALRYTKVPOVST 420
 QY 421 PTIVEYSRNLGKVGSCKKHPPEAKMCAEYLSVNLNOLCYLHEKTPSDRVTKCCTES 480
 Db 421 PTIVEYSRNLGKVGSCKKHPPEAKMCAEYLSVNLNOLCYLHEKTPSDRVTKCCTES 480
 QY 481 LYNNRPPFSALEVDTYKPKENAEETFADICLTSKEROKTKOTAYLVELYKHKPRT 540
 Db 481 LYNNRPPFSALEVDTYKPKENAEETFADICLTSKEROKTKOTAYLVELYKHKPRT 540
 QY 541 KEQKATADPAAVTEKCOAKADKEQFAEGKKVLAASQALGL 585
 Db 541 KEQKATADPAAVTEKCOAKADKEQFAEGKKVLAASQALGL 585
 RESULT 4
 US-08-797-689-2
 ; Sequence 2, Application US/08797689
 ; Patent No. 5876969
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleer, Reinhard
 ; APPLICANT: Fournier, Alain
 ; APPLICANT: Guittion, Jean-Dominique
 ; APPLICANT: Jung, Gerard
 ; APPLICANT: Yen, Patrice
 ; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 ; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.1 (PatentIn)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/797,689
 ; FILING DATE: 31-JAN-1997
 ; CLASSIFICATION NUMBER: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: FR 92/01064
 ; FILING DATE: 28-JUL-1994
 ; APPLICATION NUMBER: PCT/FR93/00085
 ; FILING DATE: 28-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith Ph.D., Julie K.
 ; REGISTRATION NUMBER: P-38-619
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3839
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 610 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-797-689-2

Query Match 100.0%; Score 3103; DB 2; Length 610;
 Best Local Similarity 100.0%; Pred. No. 9.8e-287;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAHKSEVAHFKDILGREENFKALVIAAPQYLOQCPEDHVKLYNEVTEFAKTCVADESAE 60
 25 DAHKSEVAHFKDILGREENFKALVIAAPQYLOQCPEDHVKLYNEVTEFAKTCVADESAE 84
 61 NCDKSLHTLFGDKLCTVATLRETYGENADCCAKOQPERNECFLQHKDDNPNLPLRVPEV 120
 85 NCDKSLHTLFGDKLCTVATLRETYGENADCCAKOQPERNECFLQHKDDNPNLPLRVPEV 144
 121 DYMCTAFAIDNEETFLKRYKAFTFAKRYKAFTFAKRYKAFTFAKRYKAFTFAKRLLP 160
 145 DYMCTAFAIDNEETFLKRYKAFTFAKRYKAFTFAKRYKAFTFAKRYKAFTFAKRLLP 204
 181 KLDLRLDEGKASSAKORLCA\$QFGERAKAWAVALSQRPKAFAEVSKLVTLIK 240
 205 KLDLRLDEGKASSAQRLCA\$QFGERAKAWAVALSQRPKAFAEVSKLVTLIK 264
 241 VETEFCHGDLLECADDRADLAKYICENODISSKLIKECKPYLEKSHCIAEVENDMPA 300
 265 VHEFCHGDLLECADDRADLAKYICENODISSKLIKECKPYLEKSHCIAEVENDMPA 324
 301 DFLPSLADEFVEKDKYNTAAEKDVLGMFLYEYARRHHDYSVTLRLAKTYETTLERC 360
 325 DFLPSLADEFVEKDKYNTAAEKDVLGMFLYEYARRHHDYSVTLRLAKTYETTLERC 384
 361 CAAADPHECYAKVDEFKPLVEPQNLKONCQELFOLGFLGYKTONALIVRTKYPQVST 420
 385 CAAADPHECYAKVDEFKPLVEPQNLKONCQELFOLGFLGYKTONALIVRTKYPQVST 444
 421 PTLYEVSRNLGRVGSKCCKHPEAKRMPGAEDLYSFLNQLCVLHEKPVSDRVTKCOTES 480
 445 PTLYEVSRNLGRVGSKCCKHPEAKRMPGAEDLYSFLNQLCVLHEKPVSDRVTKCOTES 504
 481 LVRRPCTSALEDEVDTYVPEKFAETTFHADICPLSEERQIKKQPALVELVKHKPKAT 540
 505 LVRRPCTSALEDEVDTYVPEKFAETTFHADICPLSEERQIKKQPALVELVKHKPKAT 564
 541 KEQIKAYMDDFAAFVEKCCKADDKETGFAERSKLYVAAQALGL 585
 565 KEQIKAYMDDFAAFVEKCCKADDKETGFAERSKLYVAAQALGL 609

RESULT 5
 US-08-256-938-2
 ; Sequence 2, Application US/08256938

GENERAL INFORMATION:
 APPLICANT: Yeh, Patrice
 TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
 COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
 PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: WORD 5.0 (patentin)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/256,938
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 92/01065
 FILING DATE: 31-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Goodman, Rosanne

REGISTRATION NUMBER: 32,534
 REFERENCE/DOCKET NUMBER: SP92007-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3817
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-256-938-2

Query Match 100.0%; Score 3103; DB 1; Length 783;
 Best Local Similarity 100.0%; Pred. No. 1, 4e-286;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db. 25 DAHKSEVAHFKDILGREENFKALVIAAPQYLOQCPEDHVKLYNEVTEFAKTCVADESAE 84
 QY 1 DAHKSEVAHFKDILGREENFKALVIAAPQYLOQCPEDHVKLYNEVTEFAKTCVADESAE 60
 Db. 25 DAHKSEVAHFKDILGREENFKALVIAAPQYLOQCPEDHVKLYNEVTEFAKTCVADESAE 84
 QY 61 NCDKSLHTLFGDKLCTATLRETYGEMADCCAKOQPERNECFLQHKDDNPNLPLRVPEV 120
 Db. 85 NCDKSLHTLFGDKLCTATLRETYGEMADCCAKOQPERNECFLQHKDDNPNLPLRVPEV 144
 QY 121 DVMCPTFHDEETFLKLYTEARHPFVAPELFLFKYKAATECCQADKAACLLP 180
 Db. 145 DVMCPTFHDEETFLKLYTEARHPFVAPELFLFKYKAATECCQADKAACLLP 204
 QY 181 KLDLRLDEGKASSAKORLCA\$QFGERAKAWAVALSQRPKAFAEVSKLVTLIK 240
 Db. 205 KLDLRLDEGKASSAKORLCA\$QFGERAKAWAVALSQRPKAFAEVSKLVTLIK 264
 QY 241 VHTECCHGDLLECADDRADLAKYICENODISSKLIKECKPYLEKSHCIAEVENDMPA 300
 Db. 265 VHTECCHGDLLECADDRADLAKYICENODISSKLIKECKPYLEKSHCIAEVENDMPA 324
 QY 301 DLPSLADEFVSKDVKYNAEAKDYLGMFLYETARRHPDYSVILLRLAKTYETTLERC 360
 Db. 325 DLPSLADEFVSKDVKYNAEAKDYLGMFLYETARRHPDYSVILLRLAKTYETTLERC 384
 QY 361 CAAADEHECYAKVDEFKPLVPEPQNLKONCQELFOLGFLGYKTONALIVRTKYPQVST 420
 Db. 385 CAAADEHECYAKVDEFKPLVPEPQNLKONCQELFOLGFLGYKTONALIVRTKYPQVST 444
 QY 421 PTLYEVSRNLGRVGSKCCKHPEAKRMPGAEDLYSFLNQLCVLHEKPVSDRVTKCOTES 480
 Db. 445 PTLYEVSRNLGRVGSKCCKHPEAKRMPGAEDLYSFLNQLCVLHEKPVSDRVTKCOTES 504
 QY 481 LYNNRCFCSALEDEVDTYVPEKFAETTFHADICPLSEERQIKKQPALVELVKHKPKAT 540
 Db. 505 LYNNRCFCSALEDEVDTYVPEKFAETTFHADICPLSEERQIKKQPALVELVKHKPKAT 564
 QY 541 KEQIKAYMDDFAAFVEKCCKADDKETGFAERSKLYVAAQALGL 585
 Db. 565 KEQIKAYMDDFAAFVEKCCKADDKETGFAERSKLYVAAQALGL 609

RESULT 6
 US-08-256-938-4

Sequence 4, Application US/08256938
 ; Patent No. 5665863;
 ; GENERAL INFORMATION:
 ; APPLICANT: Yeh, Patrice
 ; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
 ; COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
 ; PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: WORD 5.0 (patentin)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/256,938
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 92/01065
 ; FILING DATE: 31-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goodman, Rosanne

COUNTRY: USA
ZIP: 19436
COMPUTER READABLE FORM:
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,938
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/01065
FILING DATE: 31-TAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: ST92007-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3817
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
TYPE: amino acid
MOLECULE TYPE: Protein
US-08/256,938-4

Query Match 100.0%; Score 3103; DB 1; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.4e 286;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFDLGENEKFALVIAFQYQLOQCPPEDKLYNEVTFEFACTVADSEAE 60
203 DAHKSEVAHFDLGENEKFALVIAFQYQLOQCPPEDKLYNEVTFEFACTVADSEAE 262
QY 61 NCDSLEPLFGDLCPVATEPREGMADCCAKQEPERNECFLQHKDNPPLPRVPEY 120
263 NCDSLHLTFGDLCPVATEPREGMADCCAKQEPERNECFLQHKDNPPLPRVPEY 322
QY 121 DVMCTAHDNEETFLKLYELIAARRHPPFYAPELLFFAKRYKAFTTECCQADKACLLP 180
323 DVMCTAHDNEETFLKLYELIAARRHPPFYAPELLFFAKRYKAFTTECCQADKACLLP 382
QY 181 KLDLDRDEKAASSAKQRLKASLQKGERAFAWARYLISQRFKKAFTTECCQADKACLLP 240
383 KLDLDRDEKAASSAKQRLKASLQKGERAFAWARYLISQRFKKAFTTECCQADKACLLP 442
QY 241 VHTECQCHGSLLECADDPADLAKYCENODISSKKECCCPKLEKSHCTADEVENDMPA 300
443 VHTECQCHGSLLECADDPADLAKYCENODISSKKECCCPKLEKSHCTADEVENDMPA 502
QY 301 DLPSLAADFEVSKDVCKNRYAKAFQVGMFLTEYARRHPPDYSTVLLRLAKTYETLKEC 360
503 DLPSLAADFEVSKDVCKNRYAKAFQVGMFLTEYARRHPPDYSTVLLRLAKTYETLKEC 562
QY 361 CAAADPHETCKYTFDEKPKLYVEPONLKLONCEFEGLEYKFKONALVYTKVQYST 420
563 CAAADPHETCKYTFDEKPKLYVEPONLKLONCEFEGLEYKFKONALVYTKVQYST 622
Db 421 PTLYEVSRNLGKYGSKCCKPKPEAKRMPCAEDYLTSYVNLNOLCVLHEKTPVSDRVTKCTES 480
623 PTLYEVSRNLGKYGSKCCKPKPEAKRMPCAEDYLTSYVNLNOLCVLHEKTPVSDRVTKCTES 682
QY 481 LYNRPCFSALEYDETVPKFENATFPHADICLSEKEKQIKKQTKVYKHPKAT 540
683 LYNRPCFSALEYDETVPKFENATFPHADICLSEKEKQIKKQTKVYKHPKAT 742
QY 541 KEQLKAVMDDFAAFVERCKADDKETCPEEGKLYVVASQALGL 585
743 KEQLKAVMDDFAAFVERCKADDKETCPEEGKLYVVASQALGL 787

QY 1 DAHKSEVAHFDLGENEKFALVIAFQYQLOQCPPEDKLYNEVTFEFACTVADSEAE 60
203 DAHKSEVAHFDLGENEKFALVIAFQYQLOQCPPEDKLYNEVTFEFACTVADSEAE 262
QY 61 NCDSLHLTFGDLCPVATEPREGMADCCAKQEPERNECFLQHKDNPPLPRVPEY 120
263 NCDSLHLTFGDLCPVATEPREGMADCCAKQEPERNECFLQHKDNPPLPRVPEY 322
QY 121 DVMCAHDNEETFLKLYELIAARRHPPFYAPELLFFAKRYKAFTTECCQADKACLLP 180
323 DVMCAHDNEETFLKLYELIAARRHPPFYAPELLFFAKRYKAFTTECCQADKACLLP 382
QY 181 KLDLDRDEKAASSAKQRLKASLQKGERAFAWARYLISQRFKKAFTTECCQADKACLLP 240
383 KLDLDRDEKAASSAKQRLKASLQKGERAFAWARYLISQRFKKAFTTECCQADKACLLP 442

241 VHEPCCCHGDLLECAADDRAKTYCENODSTS KLIKECOKPLKEKSHCIAEVENDEMA 300
 443 VHEPCCCHGDLLECAADDRAKTYCENODSTS KLIKECOKPLKEKSHCIAEVENDEMA 502
 301 DLPSLAADFVSESKDCKNAYAARDVFLGMLFYEARHEDPSYVSLRLAKTYETTLKC 360
 503 DLPSLAADFVSESKDCKNAYAARDVFLGMLFYEARHEDPSYVSLRLAKTYETTLKC 562
 361 CAADPHCAYAKVDFSKPALKYEFBQNLKQNCELFLGMLFYEARHEDPSYVSLRLAKTYETTLKC 420
 563 CAADPHCAYAKVDFSKPALKYEFBQNLKQNCELFLGMLFYEARHEDPSYVSLRLAKTYETTLKC 622
 421 PTLYEVSNLGRGVGRCCKKPEAKRMPCAEDLSTYVLNOLCVLHEKTPVSDRVTCGES 480
 623 PTLYEVSNLGRGVGRCCKKPEAKRMPCAEDLSTYVLNOLCVLHEKTPVSDRVTCGES 682
 481 LYNRPCPSALEVDETYVPEKENAETTEFHADICLSEKERQIKKOTPAFLVLYKHKPKAT 540
 683 LYNRPCPSALEVDETYVPEKENAETTEFHADICLSEKERQIKKOTPAFLVLYKHKPKAT 742
 QY 541 KEQIKAYMDDPAAFTYKCKKADDKETCFAAECKKLYVAAQALGL 585
 Db 743 KEQIKAYMDDPAAFTYKCKKADDKETCFAAECKKLYVAAQALGL 787

RESULT 8
 US-08-222-619-3
 ; Sequence 3, Application US/08222619
 ; Patent No. 565252
 ; GENERAL INFORMATION:
 ; APPLICANT: Lichenstein, Henri
 ; APPLICANT: Lyons, David
 ; APPLICANT: Wright, Samuel
 ; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Center, Patent Operations/RRC
 ; STREET: 1840 DeHaylland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: U.S.
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/222,619
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 609 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein

US-08-222-619-3
 Query Match 99.9% Score 3099; DB:1; Length 609;
 Best Local Similarity 99.8%; Fred. No. 2.4e-286;
 Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVARFRDGEENFKALVLAFAQYLOQCPEDHYKLVNEVETRATCVADESAE 60
 Db 25 DAHKSEVARFRDGEENFKALVLAFAQYLOQCPEDHYKLVNEVETRATCVADESAE 84
 QY 61 NCDKSLHTLFGDKLCTYATLRETYGEMADCCAKQEPERNECFLQHKDNPNLPRYPERV 120

85 NCDKSLHTLFGDKLCTYATLRETYGEMADCCAKQEPERNECFLQHKDNPNLPRYPERV 144
 QY 121 DVKCTAFAIDNEETFLKLYELIARRHPTYAPELLEFAKRYKAFTECQQAIDKACLL 180
 Db 145 DVKCTAFAIDNEETFLKLYELIARRHPTYAPELLEFAKRYKAFTECQQAIDKACLL 204
 QY 181 KLDLRDGEKASSAKORLCAASLQKGERAKAWAVARLQSRPQKPAEYKSLVDTLK 240
 Db 205 KLDLRDGEKASSAKORLCAASLQKGERAKAWAVARLQSRPQKPAEYKSLVDTLK 264
 QY 241 VHTECCHGDLLECAADDRAKTYCENODSTS KLIKECOKPLKEKSHCIAEVENDEMA 300
 Db 265 VHTECCHGDLLECAADDRAKTYCENODSTS KLIKECOKPLKEKSHCIAEVENDEMA 324
 QY 301 DLPSLAADFVEYESKDVKNYKAFAKUVFQMFLEYEARHHDYSYVLLIRAKTYETTLKC 360
 Db 325 DLPSLAADFVEKDYKNTAEAKDVFGLMELTEYARHHDYSYVLLIRAKTYETTLKC 384
 QY 361 CAADPHCAYAKVDFSKPALKYEFBQNLKQNCELFLGMLFYEARHEDPSYVSLRLAKTYETTLKC 420
 Db 385 CAADPHCAYAKVDFSKPALKYEFBQNLKQNCELFLGMLFYEARHEDPSYVSLRLAKTYETTLKC 444
 QY 421 PTLYEVSNLGRGVGRCCKKPEAKRMPCAEDLSTYVLNOLCVLHEKTPVSDRVTCGES 480
 Db 445 PTLYEVSNLGRGVGRCCKKPEAKRMPCAEDLSTYVLNOLCVLHEKTPVSDRVTCGES 504
 QY 481 LYNRPCPSALEVDETYVPEKENAETTEFHADICLSEKERQIKKOTPAFLVLYKHKPKAT 540
 Db 505 LYNRPCPSALEVDETYVPEKENAETTEFHADICLSEKERQIKKOTPAFLVLYKHKPKAT 585
 QY 541 KEQIKAYMDDPAAFTYKCKKADDKETCFAAECKKLYVAAQALGL 585
 Db 565 KEQIKAYMDDPAAFTYKCKKADDKETCFAAECKKLYVAAQALGL 609

RESULT 9
 US-08-433-037-4
 ; Sequence 4, Application US/08433037
 ; Patent No. 5707888
 ; GENERAL INFORMATION:
 ; APPLICANT: Sreekrishna, Kotikanyadan
 ; APPLICANT: Barr, Kathryn A.
 ; APPLICANT: Brietley, Russell A.
 ; APPLICANT: Thill, Gregory P.
 ; APPLICANT: Tschoop, Juerg F.
 ; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/433,037
 ; FILING DATE: 03-MAY-1995
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 609 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein

Query Match 99.9% Score 3099; DB:1; Length 609;
 Best Local Similarity 99.8%; Fred. No. 2.4e-286;
 Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVARFRDGEENFKALVLAFAQYLOQCPEDHYKLVNEVETRATCVADESAE 60
 Db 25 DAHKSEVARFRDGEENFKALVLAFAQYLOQCPEDHYKLVNEVETRATCVADESAE 84
 QY 61 NCDKSLHTLFGDKLCTYATLRETYGEMADCCAKQEPERNECFLQHKDNPNLPRYPERV 120

ATTORNEY/AGENT INFORMATION: NAME: DIGIANT, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 9108Z
 TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-43-037-4

Query Match 99.9%; Score 3099; DB 4; Length 609;
; Best Local Similarity 99.8%; Pred. No. 2.4e-286; 1: Mismatches 0; Indels 0; Gaps 0;
; Matches 584; Conservative 1;

QY 1 DAHKSEVAHFKDGEENFKALVLAFAQYLQOOPFEDHVKLVNEYTERAKTCVADSAE 60
; Db 25 DAHKSEVAHFKDGEENFKALVLAFAQYLQOOPFEDHVKLVNEYTERAKTCVADSAE 84
; Db 61 NCDSL5HTLFGDKLCTVATLRETYGEMADCACAKOPERNECFLQHQDDNPNPLVREY 120
; Db 85 NCDSL5HTLFGDKLCTVATLRETYGEMADCACAKOPERNECFLQHQDDNPNPLVREY 144
; Db 121 DYNCTAHDNEETFLKYLIELARRHYYFAPELLFFAKRYKAFFTECCOAADAACLLP 180
; Db 145 DYACTAHDNEETFLKYLIELARRHYYFAPELLFFAKRYKAFFTECCOAADAACLLP 204
; Db 181 KLDLDRGKASSAKQRLKCASTLQKGERAKVANAVARLSORPKAFAEVSKLYTDLTK 240
; Db 205 KLDLDRGKASSAKQRLKCASTLQKGERAKVANAVARLSORPKAFAEVSKLYTDLTK 264
; Db 241 VHEECHGDLLECADRADLAKTYCENODSSKKLKECOKPLLESCFAEVENDMPA 300
; Db 265 VHEECHGDLLECADRADLAKTYCENODSSKKLKECOKPLLESCFAEVENDMPA 324
; Db 301 DLPSLADEFVSKDVCKNVAEAKDVFGLMFLYEARRHDPDSVLLRLAKTYETTLKC 360
; Db 325 DLPSLADEFVSKDVCKNVAEADVFGLMFLYEARRHDPDSVLLRLAKTYETTLKC 384
; Db 361 CAAADPHECYAKVDEFKPLVVEPONLLIKONCELPEQOLGEYKQNALLVRYTKVPOYST 420
; Db 385 CAAADPHECYAKVDEFKPLVVEPONLLIKONCELPEQOLGEYKQNALLVRYTKVPOYST 444
; Db 421 PTLEVYSRNLKGSKCCKHPEAKRMCAEIDLSTYLNQLCVHEKTPSDRVTKCCFES 480
; Db 445 PTLEVYSRNLKGSKCCKHPEAKRMCAEIDLSTYLNQLCVHEKTPSDRVTKCCFES 504
; Db 481 LVNRPCEPSALEDETYYKEFNAETTFHADICLSEKERQIKKQTALEVVKPKAT 540
; Db 505 LVNRPCEPSALEDETYYKEFNAETTFHADICLSEKERQIKKQTALEVVKPKAT 564
; Db 541 KEQLKAYMDDFAFVHKCCAKDDEKTCFAE9GKLVAAQALGL 585
; Db 565 KEQLKAYMDDFAFVHKCCAKDDEKTCFAE9GKLVAAQALGL 609
; RESULT 10
; US-08-897-956A-2
; Sequence 2, Application US/08897956A.
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Gram
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-08-897-956A-2

Query Match 99.9%; Score 3099; DB 4; Length 609;
; Best Local Similarity 99.8%; Pred. No. 2.4e-286; 1: Mismatches 0; Indels 0; Gaps 0;
; Matches 584; Conservative 1;

QY 1 DAHKSEVAHFKDGEENFKALVLAFAQYLQOOPFEDHVKLVNEYTERAKTCVADSAE 60
; Db 25 DAHKSEVAHFKDGEENFKALVLAFAQYLQOOPFEDHVKLVNEYTERAKTCVADSAE 84
; Db 61 NCDSL5HTLFGDKLCTVATLRETYGEMADCACAKOPERNECFLQHQDDNPNPLVREY 120
; Db 85 NCDSL5HTLFGDKLCTVATLRETYGEMADCACAKOPERNECFLQHQDDNPNPLVREY 144
; Db 121 DYNCTAHDNEETFLKYLIELARRHYYFAPELLFFAKRYKAFFTECCOAADAACLLP 180
; Db 145 DYACTAHDNEETFLKYLIELARRHYYFAPELLFFAKRYKAFFTECCOAADAACLLP 204
; Db 181 KLDLDRGKASSAKQRLKCASTLQKGERAKVANAVARLSORPKAFAEVSKLYTDLTK 240
; Db 205 KLDLDRGKASSAKQRLKCASTLQKGERAKVANAVARLSORPKAFAEVSKLYTDLTK 264
; Db 241 VHEECHGDLLECADRADLAKTYCENODSSKKLKECOKPLLESCFAEVENDMPA 300
; Db 265 VHEECHGDLLECADRADLAKTYCENODSSKKLKECOKPLLESCFAEVENDMPA 324
; Db 301 DLPSLADEFVSKDVCKNVAEAKDVFGLMFLYEARRHDPDSVLLRLAKTYETTLKC 360
; Db 325 DLPSLADEFVSKDVCKNVAEADVFGLMFLYEARRHDPDSVLLRLAKTYETTLKC 384
; Db 361 CAAADPHECYAKVDEFKPLVVEPONLLIKONCELPEQOLGEYKQNALLVRYTKVPOYST 420
; Db 385 CAAADPHECYAKVDEFKPLVVEPONLLIKONCELPEQOLGEYKQNALLVRYTKVPOYST 444
; Db 421 PTLEVYSRNLKGSKCCKHPEAKRMCAEIDLSTYLNQLCVHEKTPSDRVTKCCFES 480
; Db 445 PTLEVYSRNLKGSKCCKHPEAKRMCAEIDLSTYLNQLCVHEKTPSDRVTKCCFES 504
; Db 481 LVNRPCEPSALEDETYYKEFNAETTFHADICLSEKERQIKKQTALEVVKPKAT 540
; Db 505 LVNRPCEPSALEDETYYKEFNAETTFHADICLSEKERQIKKQTALEVVKPKAT 564
; Db 541 KEQLKAYMDDFAFVHKCCAKDDEKTCFAE9GKLVAAQALGL 585
; Db 565 KEQLKAYMDDFAFVHKCCAKDDEKTCFAE9GKLVAAQALGL 609
; RESULT 11
; US-08-897-956A-2
; Sequence 3, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: Amanin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 De Havilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids

US-08-897-956A-3

TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 PCT-US95-04075-3

Query Match 99.9%; Score 3099; DB 5; Length 609;
 Best Local Similarity 99.8%; Pred. No. 2, 4e-286;
 Matches 584; Conservative 1; Mismatches 0; Gaps 0;

1 DAHKSEYAHRFKDGEENFKALVLIATFAQYLOQCPEDHYKLYNEVTEFAKTCVADESAE 60
 25 DAHKSEYAHRFKDGEENFKALVLIATFAQYLOQCPEDHYKLYNEVTEFAKTCVADESAE 84
 61 NCDKSLHTLFGDKLCLTIVATLRETYGEMADCCAKQEPERNFCFLQHKDDNPPLPRYPEV 120
 85 NCDKSLHTLFGDKLCLTIVATLRETYGEMADCCAKQEPERNFCFLQHKDDNPPLPRYPEV 144
 121 DVACTAHDNEETFLKKLYETIARHPPYADELLFAKYKAFTTECQADKAACLLP 180
 145 DVACTAHDNEETFLKKLYETIARHPPYADELLFAKYKAFTTECQADKAACLLP 204
 181 KLDLRLDGKASSAKORLKASLQKGERAKWAVALSRQFKAFAEVSKLVIDLTK 240
 205 KLDLRLDGKASSAKORLKASLQKGERAKWAVALSRQFKAFAEVSKLVIDLTK 264
 241 VHETCCHGDLICADDRADLAKYICENODSISSKKECCKPLLEKSHCIAEVENDEMPA 300
 265 VHETCCHGDLICADDRADLAKYICENODSISSKKECCKPLLEKSHCIAEVENDEMPA 324
 301 DPLSLADEFVKYDFEKFPLVYEEQNLKQNCELFQLGEGKFKONALLYRITKKVPOYST 360
 325 DPLSLADEFVKYDFKVNCKNTAAEKDYLFLMFLYEEYARHPPYDFSVVILLRIAKTYETLEKC 384
 361 CAAADPHFCYAKVEDEKFPLVYEEQNLKQNCELFQLGEGKFKONALLYRITKKVPOYST 420
 385 CAAADPHFCYAKVEDEKFPLVYEEQNLKQNCELFQLGEGKFKONALLYRITKKVPOYST 444
 421 PTLVEVRNLGVSGKCCKEPKRMPGAEDYLSVVLNQLCVLHKTPVSDRTKCCTES 480
 445 PTLVEVRNLGVSGKCCKEPKRMPGAEDYLSVVLNQLCVLHKTPVSDRTKCCTES 504
 481 LVNRPFCSALEDEYYPKFENAEETFHADICLTSSEKERQIKKQTALEVLYKHKPKAT 540
 505 LVNRPFCSALEDEYYPKFENAEETFHADICLTSSEKERQIKKQTALEVLYKHKPKAT 564
 541 KEQLKAVMDDEFAVEKCKKADKRETCFAEGKLVYASQALGL 585
 565 KEQLKAVMDDEFAVEKCKKADKRETCFAEGKLVYASQALGL 609

RESULT 12
 US-08-897-956A-3
 Sequence 3, Application US/08897956A
 / Patent No. 6423512
 / GENERAL INFORMATION:
 / APPLICANT: Mary Ellen Digan
 / APPLICANT: Philip Lake
 / APPLICANT: Hermann Gram
 / TITLE OF INVENTION: Fusion Polypeptides
 / FILE REFERENCE: 600-7244/CPA
 / CURRENT APPLICATION NUMBER: US/08/897,956A
 / CURRENT FILING DATE: 1997-07-21
 / PRIOR APPLICATION NUMBER: 60/022,689
 / PRIOR FILING DATE: 1996-07-26
 / NUMBER OF SEQ ID NOS: 38
 / LENGTH: 978
 / TYPE: PRT
 / SOFTWARE: fastSEQ for Windows Version 4.0
 / SEQ ID NO 3
 / ORGANISM: Artificial Sequence
 / FRAGMENT:
 / OTHER INFORMATION: Fusion polypeptide

Query Match 99.7%; Score 3095; DB 4; Length 978;
 Best Local Similarity 99.8%; Pred. No. 1,1e-285;
 Matches 583; Conservative 1; Mismatches 0; Gaps 0;

1 DAHKSEYAHRFKDGEENFKALVLIATFAQYLOQCPEDHYKLYNEVTEFAKTCVADESAE 60
 212 DAHKSEYAHRFKDGEENFKALVLIATFAQYLOQCPEDHYKLYNEVTEFAKTCVADESAE 271
 61 NCDKSLHTLFGDKLCLTIVATLRETYGEMADCCAKQEPERNFCFLQHKDDNPPLPRYPEV 120
 272 NCDKSLHTLFGDKLCLTIVATLRETYGEMADCCAKQEPERNFCFLQHKDDNPPLPRYPEV 331
 121 DVACTAHDNEETFLKKLYETIARHPPYADELLFAKYKAFTTECQADKAACLLP 180
 332 DVACTAHDNEETFLKKLYETIARHPPYADELLFAKYKAFTTECQADKAACLLP 391
 181 KLDLRLDGKASSAKORLKASLQKGERAKWAVALSRQFKAFAEVSKLVIDLTK 240
 392 KLDLRLDGKASSAKORLKASLQKGERAKWAVALSRQFKAFAEVSKLVIDLTK 451
 241 VHETCCHGDLICADDRADLAKYICENODSISSKKECCKPLLEKSHCIAEVENDEMPA 300
 452 VHETCCHGDLICADDRADLAKYICENODSISSKKECCKPLLEKSHCIAEVENDEMPA 511
 301 DPLSLADEFVKYDFEKFPLVYEEQNLKQNCELFQLGEGKFKONALLYRITKKVPOYST 360
 512 DPLSLADEFVKYDFKVNCKNTAAEKDYLFLMFLYEEYARHPPYDFSVVILLRIAKTYETLEKC 571
 361 CAAADPHFCYAKVEDEKFPLVYEEQNLKQNCELFQLGEGKFKONALLYRITKKVPOYST 420
 572 CAAADPHFCYAKVEDEKFPLVYEEQNLKQNCELFQLGEGKFKONALLYRITKKVPOYST 631
 421 PTLVEVRNLGVSGKCCKEPKRMPGAEDYLSVVLNQLCVLHKTPVSDRTKCCTES 480
 632 PTLVEVRNLGVSGKCCKEPKRMPGAEDYLSVVLNQLCVLHKTPVSDRTKCCTES 691
 481 LVNRPFCSALEDEYYPKFENAEETFHADICLTSSEKERQIKKQTALEVLYKHKPKAT 540
 692 LVNRPFCSALEDEYYPKFENAEETFHADICLTSSEKERQIKKQTALEVLYKHKPKAT 751
 RESULT 13
 US-08-448-196A-3
 Sequence 3, Application US/08448196A
 / Patent No. 5780594
 / GENERAL INFORMATION:
 / APPLICANT: CARTER, DANIEL C.
 / TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
 / TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN O
 / TITLE OF INVENTION: RELATED PROTEINS
 / NUMBER OF SEQUENCES: 9
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: NASA
 / STREET: MARSHALL SPACE FLIGHT CENTER
 / CITY: HUNTSVILLE
 / STATE: ALABAMA
 / COUNTRY: USA
 / ZIP: 35812
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/448-196A
 / FILING DATE: 23-May-1995
 / CLASSIFICATION: 510
 / CLASSIFICATION: 510

```

FILE REFERENCE: 08/984,176
; CURRENT APPLICATION NUMBER: US/08/984,176
; CURRENT FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-984-176-1

Query Match 99.7%; Score: 3093; DB: 2; Length: 585;
Best Local Similarity 99.7%; Pred. No. 8.3e-286;
Matches 583; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          1 DAHKSEYAHRFKDGLBENPKALVIAFAQYILOCQPFEDHYKLVNNTEFARTCYADESAE 60
Db          1 DAHKSEYAHRFKDGLBENPKALVIAFAQYILOCQPFEDHYKLVNNTEFARTCYADESAE 60
QY          61 NCDDKSHTLFGDKLCTVATLRETYGEMDCCAKQEPERNECFLQHDDDNPLPVLVPEY 120
Db          61 NCDDKSHTLFGDKLCTVATLRETYGEMDCCAKQEPERNECFLQHDDDNPLPVLVPEY 120
QY          121 DYMCTAAPHDNEETFLKKLYIRNAPPHYAPPELLFAKYYKAATETECCQADAKAACLIP 180
Db          121 DYMCTAAPHDNEETFLKKLYIRNAPPHYAPPELLFAKYYKAATETECCQADAKAACLIP 180
QY          181 KLDDELREPGKASSAKORLKAQSLQKGGERAFAWARYLISORPKEAFAEVSKLYTDLT 240
Db          181 KLDDELREPGKASSAKORLKAQSLQKGGERAFAWARYLISORPKEAFAEVSKLYTDLT 240
QY          241 VHEPCCGDLLECADDRDLAKYICENODISSKKECCPPLKSHCTAEVENDEMPA 300
Db          241 VHEPCCGDLLECADDRDLAKYICENODISSKKECCPPLKSHCTAEVENDEMPA 300
QY          301 DFLPSLAADFVEKSYDQCKNAYAFAKDVYLGMLVEYARHPDYSVYVILRLAKTYETTEFLKC 360
Db          301 DFLPSLAADFVEKSYDQCKNAYAFAKDVYLGMLVEYARHPDYSVYVILRLAKTYETTEFLKC 360
QY          361 CARADPHECYAKVDFEKFPLVVEPQNLIKQNCELEFOLGEYKFQNQNLLYRYTKVQVYST 420
Db          361 CARADPHECYAKVDFEKFPLVVEPQNLIKQNCELEFOLGEYKFQNQNLLYRYTKVQVYST 420
QY          421 PTLYEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSVVLNQCLHLERTPYSDRYTKCCTES 480
Db          421 PTLYEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSVVLNQCLHLERTPYSDRYTKCCTES 480
QY          481 LYNRPGFESALEVDIETYVPKFEENAEETEFAHADICLSEKEQRIKQKTALEYVHKPKAT 540
Db          481 LYNRPGFESALEVDIETYVPKFEENAEETEFAHADICLSEKEQRIKQKTALEYVHKPKAT 540
QY          541 KEQKIAVADDFRAFEVKCADDKETCPAEGKKLVVASQAGL 585
Db          541 KEQKIAVADDFRAFEVKCADDKETCPAEGKKLVVASQAGL 585

RESULT 15
US-08-448-196A-5
; Sequence 5, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARRIER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: RELATED PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIPP: 35812
;
```

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/448,196A
 FILING DATE: 23-MAY-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: BROD JR, ROBERT L.
 REGISTRATION NUMBER: 18,757
 REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 205-544-0021
 TELEFAX: 205-544-0258
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 583 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-448-196A-5

Query Match 79.2%; Score 2458.5; DB 1; Length 583;
 Best Local Similarity 75.8%; Pred. No. 2.e-125;
 Matches 442; Conservative 70; Mismatches 70; Indels 1; Gaps 1;

QY 1 DAHKSEVAIRFKDILCKTVALTIRETYGEMACCAKQEPERNECFLQKDDNPNLPRVPEV 120
 Db 1 DTHKSEIAFRENDLGEKHFKGLVLYAFSOLQCPEDHVKLVNEVTEFAKKCAADESAE 60
 QY 61 NCDKSLHTLFGDKLCKTVALTIRETYGEMACCAKQEPERNECFLQKDDNPNLPRVPEV 120
 Db 61 NCDKSLHTLFGDKLCKTVALTIRETYGEMACCAKQEPERNECFLQKDDNPNLPLKL-KPEP 119
 QY 121 DYMCTAFAHDEEEFLKLYLEIARHPTEYAAPLLFAKRYKAFTECQQAADKAALLP 180
 Db 120 DAQCAAFQDDEFLGFLYLYVARHPTEYAAPLLFAKRYKAFTECQQAADKAALLP 179
 QY 181 KLDLRLDEGKASSAKQRIKKAASLQFGERAFKAWAARLSORFKAERAEVSKLVDLTK 240
 Db 180 KLDALKERLILSSAKERLKCSSFQNGEAKWAVSARLSSQKFPKAADPAEVSKVUDLTK 239
 QY 241 VHETECHGDLLECAADDRADLKYIGENODISSSRLKCCERPLERSHQJAEVENDMPA 300
 Db 240 VHEKECHGDLLECAADDRADLKYICEHQDISSSKLRKACCDKPLQKSHCIAEVKEDDLPS 299
 QY 301 DLPSLAADPCTRTVEDQPTPLVVEPSSLVKNCDFLVEYDFTV 360
 Db 300 DIPALADPAEDKICHKHPDADFLGFLYLYSREHPDYSVSLLRJAKYEAITLEK 359
 QY 361 CAAADPHFETYAKVDEKFPKVPEPONLTKONCFLFOLGEYKFONVALLYRTPKVPVST 420
 Db 360 CAEADPCTRTVEDQPTPLVVEPSSLVKNCDFLVEYDFTV 419
 QY 421 PTIYEVSRNLGKVGSCKCKHDEAKMPCADYLTSVNLQCYLHEKTPYSDRTKCCOTES 480
 Db 420 PTIYEVGRLGKVGSCKLPESELPCESENHLALANRLCYLHEKTPYSEKTTKCCOTS 479
 QY 481 IVNREICFSALLEVDTYPKFENAEFFTHADICLTCSEKIQKQTALEVLYKHKPKAT 540
 Db 480 LAERRPCFSALLEDDGPVKEKEAFTFHADICLTCDEQIKQKSALAEVLYKHKPKAT 539
 QY 541 KEQLKAYMDDFAAFVCKADDKTCFAEGKQLVASSQAL 583
 Db 540 KEQLKTVLGNFSAAVAKCGREDKFACFAEGPKLVASSQAL 582

protein - protein search, using sw model		Search time 28 Seconds (without alignments)		
on on:		August 31, 2003, 16:33:53 ; Search time 28 Seconds		
title:	US-09-833-041-18	DB length:	585	
correct score:	3103	Maximum DB length:	585	
quence:	1 DAHKSEYAHRFKDGLGEENFK.....	Minimum DB length:	585	
scoring table:	BLOSUM62	Number of hits satisfying chosen parameters:	510680	
Gapop:	10.0	Gapext:	0.5	
searched:	510680 seqs, 136781880 residues	Maximum Match 100%	0%	
st-processing:	Listing first 45 summaries	Minimum Match 0%	0%	
Database :	Published_Applications_AA_*	Maximum Match 100%	0%	
	1: /cgn2_6_ptodata/2/pbpaas/US07_PUBCOMB.pep.*	Minimum Match 100%	0%	
	2: /cgn2_6_ptodata/2/pbpaas/US07_PUBCOMB.pep.*	Maximum Match 100%	0%	
	3: /cgn2_6_ptodata/2/pbpaas/US06_NEW_PUB.pep.*	Minimum Match 100%	0%	
	4: /cgn2_6_ptodata/2/pbpaas/US06_NEW_PUB.pep.*	Maximum Match 100%	0%	
	5: /cgn2_6_ptodata/2/pbpaas/US07_PUBCOMB.pep.*	Minimum Match 100%	0%	
	6: /cgn2_6_ptodata/2/pbpaas/US07_PUBCOMB.pep.*	Maximum Match 100%	0%	
	7: /cgn2_6_ptodata/2/pbpaas/US08_NEW_PUB.pep.*	Minimum Match 100%	0%	
	8: /cgn2_6_ptodata/2/pbpaas/US08_PUBCOMB.pep.*	Maximum Match 100%	0%	
	9: /cgn2_6_ptodata/2/pbpaas/US09_PUBCOMB.pep.*	Minimum Match 100%	0%	
	10: /cgn2_6_ptodata/2/pbpaas/US09_PUBCOMB.pep.*	Maximum Match 100%	0%	
	11: /cgn2_6_ptodata/2/pbpaas/US09_PUBCOMB.pep.*	Minimum Match 100%	0%	
	12: /cgn2_6_ptodata/2/pbpaas/US09_NEW_PUB.pep.*	Maximum Match 100%	0%	
	13: /cgn2_6_ptodata/2/pbpaas/US10_PUBCOMB.pep.*	Minimum Match 100%	0%	
	14: /cgn2_6_ptodata/2/pbpaas/US10_PUBCOMB.pep.*	Maximum Match 100%	0%	
	15: /cgn2_6_ptodata/2/pbpaas/US10_PUBCOMB.pep.*	Minimum Match 100%	0%	
	16: /cgn2_6_ptodata/2/pbpaas/US60_NEW_PUB.pep.*	Maximum Match 100%	0%	
	17: /cgn2_6_ptodata/2/pbpaas/US60_NEW_PUB.pep.*	Minimum Match 100%	0%	
	18: /cgn2_6_ptodata/2/pbpaas/US60_PUBCOMB.pep.*	Maximum Match 100%	0%	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.		SUMMARIES		
result No.	Score	Query Match	Length DB ID	Description
1	3103	100.0	585	US-09-929-552-2
2	3103	100.0	585	US-09-932-61-445
3	3103	100.0	585	US-09-938-010-26
4	3103	100.0	585	US-09-833-041-18
5	3103	100.0	585	US-10-153-604-5
6	3103	100.0	585	US-10-153-064-5
7	3103	100.0	604	US-09-984-010-7
8	3103	100.0	609	US-09-913-039-370
9	3103	100.0	609	US-10-153-604-7
10	3103	100.0	609	US-10-153-064-7
11	3103	100.0	610	US-09-984-186-2
12	3103	100.0	610	US-10-237-667-2
13	3103	100.0	610	US-10-237-708-2
14	3103	100.0	610	US-10-237-866-2
15	3103	100.0	610	US-10-237-871-2

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

100

Result % Query % Summaries

No.	Score	Match Length	DB ID	Description
1	31.03	100.0	585	US-09-929-552-2 Sequence 2, Appli
2	31.03	100.0	585	US-09-932-613-445 Sequence 445, Appli
3	31.03	100.0	585	US-09-984-010-26 Sequence 26, Appli
4	31.03	100.0	585	US-09-833-041-18 Sequence 18, Appli
5	31.03	100.0	585	US-10-153-504A-5 Sequence 5, Appli
6	31.03	100.0	585	US-10-153-100A-5 Sequence 5, Appli
7	31.03	100.0	604	US-09-984-010-5 Sequence 7, Appli
8	31.03	100.0	609	US-09-919-039-370 Sequence 370, Appli
9	31.03	100.0	609	US-10-153-604A-7 Sequence 7, Appli
10	31.03	100.0	609	US-10-153-064-7 Sequence 7, Appli
11	31.03	100.0	610	US-09-184-186-2 Sequence 2, Appli
12	31.03	100.0	610	US-10-237-667-2 Sequence 2, Appli
13	31.03	100.0	610	US-10-237-708-2 Sequence 2, Appli
14	31.03	100.0	610	US-10-137-866-2 Sequence 2, Appli
15	31.03	100.0	610	US-10-237-871-2 Sequence 2, Appli

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-929-552-2

Query Match 100.0%; Score 3103; DB 10; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-270;
 Matches 585; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAHKSEVAHFKLQDGKQFVAKYKAAFFTECQADAKACLLP 60
 1 DAHKSEVAHFKLQDGKQFVAKYKAAFFTECQADAKACLLP 60
 61 NCDKSLEHTLFGDKLCTVATLREYYGENADCAKQPERNECFQHKDDNPPLPRVRPEY 120
 61 NCDKSLEHTLFGDKLCTVATLREYYGENADCAKQPERNECFQHKDDNPPLPRVRPEY 120
 61 NCDKSLEHTLFGDKLCTVATLREYYGENADCAKQPERNECFQHKDDNPPLPRVRPEY 120
 121 DYMCTAHDNEETFLKKLYEIAARRHFFYAPELLFFAKRYKAAFFTECQADAKACLLP 180
 121 DYMCTAHDNEETFLKKLYEIAARRHFFYAPELLFFAKRYKAAFFTECQADAKACLLP 180
 181 KLDLRDEGKASSAKORLKCASTQKGERAKFKAVALSRQFFKAAFFPAEVSKLYDLFK 240
 181 KLDLRDEGKASSAKORLKCASTQKGERAKFKAVALSRQFFKAAFFPAEVSKLYDLFK 240
 121 DYMCTAHDNEETFLKKLYEIAARRHFFYAPELLFFAKRYKAAFFTECQADAKACLLP 180
 121 DYMCTAHDNEETFLKKLYEIAARRHFFYAPELLFFAKRYKAAFFTECQADAKACLLP 180
 181 KLDLRDEGKASSAKORLKCASTQKGERAKFKAVALSRQFFKAAFFPAEVSKLYDLFK 240
 181 KLDLRDEGKASSAKORLKCASTQKGERAKFKAVALSRQFFKAAFFPAEVSKLYDLFK 240
 241 VHTECGHDILECADDRADLAKYICENODSSKKLKECCCKPLKESKCIAYEVNDEMPA 300
 241 VHTECGHDILECADDRADLAKYICENODSSKKLKECCCKPLKESKCIAYEVNDEMPA 300
 361 CAAADPHECYAKVDEFPKLVEPQNLIKONCEPQLGKPFKONALIYRVTKKVQVST 420
 361 CAAADPHECYAKVDEFPKLVEPQNLIKONCEPQLGKPFKONALIYRVTKKVQVST 420
 301 DPLSTAADFVEPSDKVCKNYAAEKDVLIGMFLYETARRHFDYSTVLLRLAKYETLERC 360
 301 DPLSTAADFVEPSDKVCKNYAAEKDVLIGMFLYETARRHFDYSTVLLRLAKYETLERC 360
 361 CAAADPHECYAKVDEFPKLVEPQNLIKONCEPQLGKPFKONALIYRVTKKVQVST 420
 361 CAAADPHECYAKVDEFPKLVEPQNLIKONCEPQLGKPFKONALIYRVTKKVQVST 420
 421 PTIVYEVSRNLGKVSKCCKHPEAKRMPKAEDYLSTYVLNOLCVLHEKTPVSDRVTKCCTES 480
 421 PTIVYEVSRNLGKVSKCCKHPEAKRMPKAEDYLSTYVLNOLCVLHEKTPVSDRVTKCCTES 480
 421 PTIVYEVSRNLGKVSKCCKHPEAKRMPKAEDYLSTYVLNOLCVLHEKTPVSDRVTKCCTES 480
 481 IYNRPRPCSALEDTETYVKENAEKTFHADICLTSERKQIKKQTALEVLYKHKPKAT 540
 481 IYNRPRPCSALEDTETYVKENAEKTFHADICLTSERKQIKKQTALEVLYKHKPKAT 540
 541 KEQLKAVMDFAAFVEKCCAKDDEKTFCAEGKKLVAAASQALG 585
 541 KEQLKAVMDFAAFVEKCCAKDDEKTFCAEGKKLVAAASQALG 585
 RESULT 2
 US-09-932-613-445
 ; Sequence 445, Application US/09932613
 ; Publication No. US20030091565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; APPLICANT: Beltzner, James P.
 ; APPLICANT: Potter, M. Daniel
 ; APPLICANT: Fleming, Tony J.
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 ; FILE REFERENCE: DXY-025.1 PCT; DXY-025.1 US
 ; CURRENT APPLICATION NUMBER: US/09/932,613
 ; CURRENT FILING DATE: 2001-08-17
 ; NUMBER OF SEQ ID NOS: 458
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO: 445
 ; LENGTH: 585
 ; TYPE: PCT
 ; ORGANISM: HomoSapiens
 ; RESULT 2
 US-09-932-613-445
 ; Sequence 445, Application US/09932613
 ; Publication No. US20030091565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; APPLICANT: Beltzner, James P.
 ; APPLICANT: Potter, M. Daniel
 ; APPLICANT: Fleming, Tony J.
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 ; FILE REFERENCE: DXY-025.1 PCT; DXY-025.1 US
 ; CURRENT APPLICATION NUMBER: US/09/932,613
 ; CURRENT FILING DATE: 2001-08-17
 ; NUMBER OF SEQ ID NOS: 458
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO: 445
 ; LENGTH: 585
 ; TYPE: PCT
 ; ORGANISM: HomoSapiens

; FILING DATE: 19-DEC-1996
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 585 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 ; us-09-984-010-26

Query Match 100.0%; Score 3103; DB 11; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-70; Mismatches 0; Gaps 0;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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  QY 1 DAHKSEYAHRFKDGLGENEENFKALVIAFAQYQLOQCPEDFHVLYNTEFAKTCYADESAE 60
  Db 1 DAHKSEYAHRFKDGLGENEENFKALVIAFAQYQLOQCPEDFHVLYNTEFAKTCYADESAE 60
  QY 61 NCOKSLSLTLEFDKLTCTVATLREYGENADCCAKQPERNECFLQHKKDDNPNLPRVRPEV 120
  Db 61 NCOKSLSLTLEFDKLTCTVATLREYGENADCCAKQPERNECFLQHKKDDNPNLPRVRPEV 120
  QY 121 DVACTAHDNNEETFLKKYIETLARRHFFYAPELLFFAKRYKAFFTECCQAAACLLP 180
  Db 121 DVACTAHDNNEETFLKKYIETLARRHFFYAPELLFFAKRYKAFFTECCQAAACLLP 180
  QY 181 KLDLERDEGKASSAKORLKCASTQKGERAKKAVARLSQREPKAFAEYSKVLTDLTK 240
  Db 181 KLDLERDEGKASSAKORLKCASTQKGERAKKAVARLSQREPKAFAEYSKVLTDLTK 240
  QY 241 VHTPCCGHDLLCADCADRALAKYTCENODISSKKLKECCPKLEKSHCIAEVENDEMA 300
  Db 241 VHTPCCGHDLLCADCADRALAKYTCENODISSKKLKECCPKLEKSHCIAEVENDEMA 300
  QY 301 DLPSIAADEVESKDYCKNTAAEKDFVQGMFLYEAARRHDPSVYLRLAKTYETTLEKC 360
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  QY 361 CAAADPHFCYAKVDFEKPLVEEFQNLIKQNCLEPQOLGKYEFLVRYTKKVQYST 420
  Db 361 CAAADPHFCYAKVDFEKPLVEEFQNLIKQNCLEPQOLGKYEFLVRYTKKVQYST 420
  QY 421 PTLYEVSNLGRVGSCKKHPKAERMPQAEDYLSTVNLQCVLHEKTPVSDRVTKCCTES 480
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  QY 481 LYNNRPCFSALEYDEYYPKFENETFHADICLSEKERQIKKQPAEDYLSTVNLQCVLHEKTPVSDRVTKCCTES 540
  Db 481 LYNNRPCFSALEYDEYYPKFENETFHADICLSEKERQIKKQPAEDYLSTVNLQCVLHEKTPVSDRVTKCCTES 540
  QY 541 KEQLKAVMDDFAAFVKCCKADDKETCPAEEGKKLVASAAGL 585
  Db 541 KEQLKAVMDDFAAFVKCCKADDKETCPAEEGKKLVASAAGL 585
  
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RESULT 5
US-10-153-604A-5

Sequence 5, Application US/10153604A
 ; Publication No. US20030143191A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PF556
 ; CURRENT APPLICATION NUMBER: US/10/153,604A
 ; CURRENT FILING DATE: 2002-05-24
 ; PRIOR APPLICATION NUMBER: 60/293,212
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 585
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens

25 DAHKSEYAHFKDGLGEENFKALYLIAPQYIQQCPFDHKLVNEYTEFAKTCVADSEAE 84
 QY 61 NCDKSLHTLLEGDKLCTVATLRETYGENMADCCAKOKEPERNECLOHDDNPLPRYREV 120
 Db 85 NCDKSLHTLLEGDKLCTVATLRETYGENMADCCAKOKEPERNECLOHDDNPLPRYREV 144
 121 DYMCTAHPDNEETFLKKLYTETARRPPYTAPELLEFAKRAAFTCCQAAKACLLP 180
 QY 145 DYMCTAHPDNEETFLKKLYTETARRPPYTAPELLEFAKRAAFTCCQAAKACLLP 204
 Db 181 KLDLRLDEGKASSAKORLCASTLQKGERAKAVARLSQLRPPKAFAEYSKVLTDLTK 240
 QY 205 KLDLRLDEGKASSAKORLCASTLQKGERAKAVARLSQLRPPKAFAEYSKVLTDLTK 264
 Db 241 VHEPCCGDLECAADRADLAKYTCENQDSISSKKECEKPELEKSHCAEVENDPMA 300
 QY 265 VHEPCCGDLECAADRADLAKYTCENQDSISSKKECEKPELEKSHCAEVENDPMA 324
 Db 301 DLPSSLADFEVKDCKNTAEADFLGFLMELYARRHDPDSVLLRLAKTYETTLERK 360
 QY 325 DLPSSLADFEVKDCKNTAEADFLGFLMELYARRHDPDSVLLRLAKTYETTLERK 384
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 Db 385 CAAADPHECYAKVDFKPLVVEFQNLKONGELFOLQGEYKONALIYRKYKPVQSP 444
 QY 421 PTLYVESRNLGRGVGSKCKHPEAKRMPAEDYLSTVNLQCVLHEKTPVSDRVTKCCTES 480
 Db 445 PTLYVESRNLGRGVGSKCKHPEAKRMPAEDYLSTVNLQCVLHEKTPVSDRVTKCCTES 504
 QY 481 LYNRPCSALEDEYYVPEKENETFFHADICLSEKERQIKKOTALVELVKHKPKAT 540
 Db 505 LYNRPCSALEDEYYVPEKENETFFHADICLSEKERQIKKOTALVELVKHKPKAT 564
 QY 541 KEOLKAVMDDEAFAVEKCKADDKETCPAEKKLVAAQALGL 585
 Db 565 KEOLKAVMDDEAFAVEKCKADDKETCPAEKKLVAAQALGL 609

RESULT 11
 US-09-984-186-2
 Sequence 2, Application US/09984186
 ; Patent No. US2002015101A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleer, Reinhard
 ; Fournier, Alain
 ; Guittot, Jean Dominique
 ; Jung, Gerard
 ; Yeh, Patrice
 ; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 ; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 ; CONTAINING SAID POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone Poulen Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.1 (PatentIn)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/984,186
 ; FILING DATE: 29-Oct-2001
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/797,689
 ; FILING DATE: 31-Jan-1997
 ; APPLICATION NUMBER: US/08/256,927
 ; FILING DATE: 28-Jul-1994
 ; APPLICATION NUMBER: FR 92/01064
 ; FILING DATE: 31-Jan-1992
 ; APPLICATION NUMBER: PCT/FR93/00085
 ; FILING DATE: 28-Jan-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, Ph.D., Julie K.
 ; REGISTRATION NUMBER: P-38,619

US-10-153-064-7
 ; Sequence 7, Application US/10153064
 ; Publication No. US20020142814A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemoquine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PP556
 ; CURRENT APPLICATION NUMBER: US/10/153,064
 ; CURRENT FILING DATE: 2002-05-24
 ; PRIORITY APPLICATION NUMBER: 60/293,212
 ; PRIORITY FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-153-064-7

Query Match 100.0%; Score 3103; DB 14; Length 609;
 Best Local Similarity 100.0%; Pred. No. 1.1e-0; Mismatches 0; Indels 0; Gaps 0;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEYAHFKDGLGEENFKALYLIAPQYIQQCPFDHKLVNEYTEFAKTCVADSEAE 60
 Db 25 DAHKSEYAHFKDGLGEENFKALYLIAPQYIQQCPFDHKLVNEYTEFAKTCVADSEAE 84
 QY 61 NCDKSLHTLLEGDKLCTVATLRETYGENMADCCAKOKEPERNECLOHDDNPLPRYREV 120
 Db 85 NCDKSLHTLLEGDKLCTVATLRETYGENMADCCAKOKEPERNECLOHDDNPLPRYREV 144
 QY 121 DYMCTAHPDNEETFLKKLYTETARRPPYTAPELLEFAKRAAFTCCQAAKACLLP 180
 |||||

REFERENCE/DOCKET NUMBER: ST92006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3808
 TELEFAX: (610) 454-3809
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-984-186-2

Query Match Score 3103; DB 10; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1.1e-270; Gaps 0;
 Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKSEVAHREFKDGEENFKALVLYIAPAQYLOQQCPEDHKLYNEVTEFAKTCVADESA 60
 25 DAKSEVAHREFKDGEENFKALVLYIAPAQYLOQQCPEDHKLYNEVTEFAKTCVADESA 84

QY 61 NCDSLETLFGDKLCTVATLRETYGENADCAKQPERNECFLQHDDNPNLPRVPRPEV 120
 85 NCDSKHTLFGDKLCTVATLRETYGENADCAKQPERNECFLQHDDNPNLPRVPRPEV 144

QY 121 DYMCTAHPDNBETFLRKLYELARHPPYFAPELFFAKRYKAFTTECCQADKAICLIP 180
 145 DVCTAHPDNBETFLRKLYELARHPPYFAPELFFAKRYKAFTTECCQADKAICLIP 204

Db 181 KLDLRLDEGKASSAKORLKCASTQKFGERAKWAVALSRQEPKAFAEVSKLVTDLTK 240
 QY 205 KLDLRLDEGKASSAKORLKCASTQKFGERAKWAVALSRQEPKAFAEVSKLVTDLTK 264

QY 241 VHFECCGDLICLCAADRAILAKTCENODSSSKKECEKPKLKEHCTADEVENDEMPA 300
 265 VHFECCGDLICLCAADRAILAKTCENODSSSKKECEKPKLKEHCTADEVENDEMPA 324

QY 301 DLPSLADEADEVSKICKNAYAKDVFGLMELYEYARRHDPSYSTVLLRLAKTYETLEKC 360
 325 DLPSLADEADEVSKICKNAYAKDVFGLMELYEYARRHDPSYSTVLLRLAKTYETLEKC 384

QY 361 CAAADPHCYAKVDFEKPVLVEPONLQKONCELEQQLGEYKQFQNALLVRPTKKPQVST 4.20
 385 CAAADPHCYAKVDFEKPVLVEPONLQKONCELEQQLGEYKQFQNALLVRPTKKPQVST 444

QY 421 PTLYEVSNLGRVSGCKKHEPEARMPAEDYLSTVLLNQCVTHKEKTPSDRVTCCTIS 480
 445 PTLYEVSNLGRVSGCKKHEPEARMPAEDYLSTVLLNQCVTHKEKTPSDRVTCCTIS 504

QY 481 LYNRPCFCSALEDYYPPKEFNAETFTFHADICLSEKEQIKKOTALVELVKHPRAT 540
 505 LVNRRPCFCSALEDYYPPKEFNAETFTFHADICLSEKEQIKKOTALVELVKHPRAT 564

QY 541 KEQKAVMDDEAFAVFKCKDADKECPTCAEFGKKLYAASOALGL 585
 565 KEQKAVMDDEAFAVFKCKDADKECPTCAEFGKKLYAASOALGL 609

RESULT 12 US-10-237-667-2
 Sequence 2, Application US/10237667
 Publication No. US2003002308A1
 GENERAL INFORMATION:
 APPLICANT: Fieer, Reinhard
 Fournier, Alain
 Ghitton, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice
 TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 CONTAINING SAID POLYPEPTIDES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3043
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/237,667
 FILING DATE: 10-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US 08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST22006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 2:
 IN INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-237-667-2

Query Match Score 3103; DB 15; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1.1e-270;
 Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKSEVAHREFKDGEENFKALVLYIAPAQYLOQQCPEDHKLYNEVTEFAKTCVADESA 60
 25 DAKSEVAHREFKDGEENFKALVLYIAPAQYLOQQCPEDHKLYNEVTEFAKTCVADESA 84

QY 61 NCDSLETLFGDKLCTVATLRETYGENADCAKQPERNECFLQHDDNPNLPRVPRPEV 120
 85 NCDSKHTLFGDKLCTVATLRETYGENADCAKQPERNECFLQHDDNPNLPRVPRPEV 144

QY 121 DYMCTAHPDNBETFLRKLYELARHPPYFAPELFFAKRYKAFTTECCQADKAICLIP 180
 145 DVCTAHPDNBETFLRKLYELARHPPYFAPELFFAKRYKAFTTECCQADKAICLIP 204

Db 181 KLDLRLDEGKASSAKORLKCASTQKFGERAKWAVALSRQEPKAFAEVSKLVTDLTK 240
 QY 205 KLDLRLDEGKASSAKORLKCASTQKFGERAKWAVALSRQEPKAFAEVSKLVTDLTK 264

QY 241 VHFECCGDLICLCAADRAILAKTCENODSSSKKECEKPKLKEHCTADEVENDEMPA 300
 265 VHFECCGDLICLCAADRAILAKTCENODSSSKKECEKPKLKEHCTADEVENDEMPA 324

QY 301 DLPSLADEADEVSKICKNAYAKDVFGLMELYEYARRHDPSYSTVLLRLAKTYETLEKC 360
 325 DLPSLADEADEVSKICKNAYAKDVFGLMELYEYARRHDPSYSTVLLRLAKTYETLEKC 384

QY 361 CAAADPHCYAKVDFEKPVLVEPONLQKONCELEQQLGEYKQFQNALLVRPTKKPQVST 4.20
 385 CAAADPHCYAKVDFEKPVLVEPONLQKONCELEQQLGEYKQFQNALLVRPTKKPQVST 444

QY 421 PTLYEVSNLGRVSGCKKHEPEARMPAEDYLSTVLLNQCVTHKEKTPSDRVTCCTIS 480
 445 PTLYEVSNLGRVSGCKKHEPEARMPAEDYLSTVLLNQCVTHKEKTPSDRVTCCTIS 504

QY 481 LYNRPCFCSALEDYYPPKEFNAETFTFHADICLSEKEQIKKOTALVELVKHPRAT 540
 505 LVNRRPCFCSALEDYYPPKEFNAETFTFHADICLSEKEQIKKOTALVELVKHPRAT 564

QY 541 KEQKAVMDDEAFAVFKCKDADKECPTCAEFGKKLYAASOALGL 585
 565 KEQKAVMDDEAFAVFKCKDADKECPTCAEFGKKLYAASOALGL 609

Db 205 KLDLRLDEGKASSAKORLKCASTQKFGERAKWAVALSRQEPKAFAEVSKLVTDLTK 240
 QY 241 VHTECHGDLLEADRADIAKTCENODSSSKKECEKPKLKEHCTADEVENDEMPA 300
 265 VHTECHGDLLEADRADIAKTCENODSSSKKECEKPKLKEHCTADEVENDEMPA 324
 QY 301 CAAADPHCYAKVDFEKPVLVEPONLQKONCELEQQLGEYKQFQNALLVRPTKKPQVST 420
 325 DLPSLADEADEVSKICKNAYAKDVFGLMELYEYARRHDPSYSTVLLRLAKTYETLEKC 384
 361 CAAADPHCYAKVDFEKPVLVEPONLQKONCELEQQLGEYKQFQNALLVRPTKKPQVST 444
 385 CAAADPHCYAKVDFEKPVLVEPONLQKONCELEQQLGEYKQFQNALLVRPTKKPQVST 444
 QY 421 PTLYEVSNLGRVSGCKKHEPEARMPAEDYLSTVLLNQCVTHKEKTPSDRVTCCTIS 480

445 PRIVEYSRNLGVGSKCCKHPEAKRMECAEDYLSVTLNCLCVLHEKTPVSDRIVKCCES 504
 481 LVNRPFAEDEVDTYVKEFAEATTEFHADICLSEERQKKQALVLEVKPKAT 540
 505 LVNRPFAEDEVDTYVKEFAEATTEFHADICLSEERQKKQALVLEVKPKAT 564
 541 KEQLKAVMDDPAATFTEKCKADDKETCFAEKGKKLVAAQALGL 585
 565 KEQLKAVMDDPAATFTEKCKADDKETCFAEKGKKLVAAQALGL 609

RESULT 13
 US-10-237-708-2
 Sequence 2, Application US/10237708
 Publication No. US20030036170A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guitton, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3043
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10-237,708
 FILING DATE: 10-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US/08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph. D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: SF92006-US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-237-708-2

Query Match 100.0% Score 3103; DB:15; Length 610;
 Best Local Similarity 100.0% pred. No. 1.1e-270;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDGLGENFKALVLIJAAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 84
 25 DAHKSEVAHRFKDGLGENFKALVLIJAAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 84
 61 NCDKSLHTEFGDKLCTATLRETGYEMADCCAKOEPFNECFLQHKDDNPFLRVPFPEV 120
 85 NCDKSLHTEFGDKLCTATLRETGYEMADCCAKOEPFNECFLQHKDDNPFLRVPFPEV 144
 121 DYMCPAFHDEERFLKLYLIAHSPYYAPELLEFAKRYKAATECCQAKAAGCILP 180
 145 DYMCPAFHDEERFLKLYLIAHSPYYAPELLEFAKRYKAATECCQAKAAGCILP 204
 181 KLDDELDEGKASSAKOPLKCASLOKFGEFAKWAVALSORPFAEAEVSKLVIDLT 240
 241 VHTECCHGDLLEADDRADILAKYICENQDSSSKLKECPLKSHCTAEVENDMPA 300
 265 VHTECCHGDLLEADDRADILAKYICENQDSSSKLKECPLKSHCTAEVENDMPA 324
 301 DLPSLAADFVEPSDVCKNYARAKDVFGLMFLYEFYARRHPDYSVWLLRLAKTYETTLEKC 360
 325 DLPSLAADFVEPSDVCKNYARAKDVFGLMFLYEFYARRHPDYSVWLLRLAKTYETTLEKC 384
 361 CAAADPHECAYKVFDEKPLVYEPQNLKONCELEFOGEYKFONALLYRTYKVPQYST 420
 385 CAAADPHECAYKVFDEKPLVYEPQNLKONCELEFOGEYKFONALLYRTYKVPQYST 444
 421 PTLVEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPSDRTYKCCTES 480
 445 PTLVEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPSDRTYKCCTES 504

QY 505 LVNRRPCFSALEDETYPKEFNAETFHADICLSEKRIKKOTALVELYTKHPKAT 540
 541 KEQLKAVMDDFAAFVCKKADDKETCFAEKGKKLVAAQALGL 585
 565 KEQLKAVMDDFAAFVCKKADDKETCFAEKGKKLVAAQALGL 609

RESULT 14
 US-10-237-866-2
 Sequence 2, Application US/10237866
 Publication No. US20030036171A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guitton, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 ZIP: 19426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10-237,866
 FILING DATE: 10-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US/08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph. D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: SF92006-US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-237-708-2

Query Match 100.0% Score 3103; DB:15; Length 610;
 Best Local Similarity 100.0% pred. No. 1.1e-270;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDGLGENFKALVLIJAAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 60

FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28 JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST92006-08
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-237-866-2

Query Match 100.0%; Score 3103; DB 15; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1.1e-270;
 Matches 565; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAHKSEYAHREPKDGEENFKALVIAPAQYIQLQCPPEDEVHLYNEVTEFAKTCVADESAE 60
 Db 25 DAHKSEYAHREPKDGEENFKALVIAPAQYIQLQCPPEDEVHLYNEVTEFAKTCVADESAE 84
 QY 61 NCDSLSELTFLGDKLCTVATLREYNGEMADCCAKOFPERNECFLQHKKDDNPNLPRVRPEY 120
 Db 85 NCDSLSELTFLGDKLCTVATLREYNGEMADCCAKOFPERNECFLQHKKDDNPNLPRVRPEY 144
 QY 121 DYNCTAPHDNEETFLKKLYEATRHYPPYAPELIFAKRYKAFAEPECCQAAADKAACCLP 180
 Db 145 DYNCTAPHDNEETFLKKLYEATRHYPPYAPELIFAKRYKAFAEPECCQAAADKAACCLP 204
 QY 181 KLDLRLDEGKASSAKURJKCASLQKGERAKWAVARLQSREPKAFATVSKLYVDTK 240
 Db 205 KLDLRLDEGKASSAKURJKCASLQKGERAKWAVARLQSREPKAFATVSKLYVDTK 264
 QY 241 VHECCCHGDLLECADDRADLAKYTCENODSSSKLKECCPKLEKSHCIAEVENDMPA 300
 Db 265 VHECCCHGDLLECADDRADLAKYTCENODSSSKLKECCPKLEKSHCIAEVENDMPA 324
 QY 301 DLSLAADEYPSKDYCKNFAEAADVEGMELYEYARREPKDYSVYLRLAKTYETTLERK 360
 Db 325 DLSLAADEYPSKDYCKNFAEAADVEGMELYEYARREPKDYSVYLRLAKTYETTLERK 384
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 Db 385 CAAADPHECYAKVDEPKPLVREQNLKONCEPEQGEYKTONALLYRKTQVYST 444
 QY 421 PTLYEVSRNLGKVSKCCKHPEAKRMPAOEYLSTVLNQLCVLHEKTPVSDRVTCKCTPS 480
 Db 445 PTLYEVSRNLGKVSKCCKHPEAKRMPAOEYLSTVLNQLCVLHEKTPVSDRVTCKCTPS 504
 QY 481 LVNRPCESALEDEVTYKEVNAETTFHADICLSETERQKKPALVPLVKEKPKAT 540
 Db 505 LVNRPCESALEDEVTYKEFNFETTFHADICLSETERQKKPALVPLVKEKPKAT 564
 QY 541 KEQLKAYMDPAAFEVKCCAKDDETCFAEBSGKKLYAASORAGL 585
 Db 565 KEQLKAYMDPAAFEVKCCAKDDETCFAEBSGKKLYAASORAGL 609

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESS: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3043
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (Patentin)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/237,871
 FILING DATE: 10-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,589
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US/08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST92006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-237-871-2

Query Match 100.0%; Score 3103; DB 15; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1.1e-270;
 Matches 585; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAHKSEVREPKDGEENFKALVIAQYIQLQCPPEDEVHLYNEVTEFAKTCVADESAE 60
 Db 25 DAHKSEVREPKDGEENFKALVIAQYIQLQCPPEDEVHLYNEVTEFAKTCVADESAE 84
 QY 61 DYNCTAPHDNEETFLKKLYEATRHYPPYAPELIFAKRYKAFAEPECCQAAADKAACCLP 120
 Db 85 NCDKSLHFLGDKLCTVATLREYNGEMADCCAKQEPERNECFLQHKKDDNPNLPRVRPEY 144
 QY 121 DYNCTAPHDNEETFLKKLYEATRHYPPYAPELIFAKRYKAFAEPECCQAAADKAACCLP 180
 Db 145 DYNCTAPHDNEETFLKKLYEATRHYPPYAPELIFAKRYKAFAEPECCQAAADKAACCLP 204
 QY 181 KLDLRLDEGKASSAKURJKCASLQKGERAKWAVARLQSREPKAFATVSKLYVDTK 240
 Db 205 KLDLRLDEGKASSAKURJKCASLQKGERAKWAVARLQSREPKAFATVSKLYVDTK 264
 QY 241 VHECCCHGDLLECADDRADLAKYTCENODSSSKLKECCPKLEKSHCIAEVENDMPA 300
 Db 265 VHECCCHGDLLECADDRADLAKYTCENODSSSKLKECCPKLEKSHCIAEVENDMPA 324
 QY 301 DLSLAADEYPSKDYCKNFAEAADVEGMELYEYARREPKDYSVYLRLAKTYETTLERK 360
 Db 325 DLSLAADEYPSKDYCKNFAEAADVEGMELYEYARREPKDYSVYLRLAKTYETTLERK 384
 QY 361 CAAADPHECYAKVDEPKPLVREQNLKONCEPEQGEYKTONALLYRKTQVYST 420
 Db 385 CAAADPHECYAKVDEPKPLVREQNLKONCEPEQGEYKTONALLYRKTQVYST 444
 QY 421 PTLYEVSRNLGKVSKCCKHPEAKRMPAOEYLSTVLNQLCVLHEKTPVSDRVTCKCTPS 480
 Db 445 PTLYEVSRNLGKVSKCCKHPEAKRMPAOEYLSTVLNQLCVLHEKTPVSDRVTCKCTPS 504
 QY 481 LVNRPCESALEDEVTYKEVNAETTFHADICLSETERQKKPALVPLVKEKPKAT 540
 Db 505 LVNRPCESALEDEVTYKEFNFETTFHADICLSETERQKKPALVPLVKEKPKAT 564
 QY 541 KEQLKAYMDPAAFEVKCCAKDDETCFAEBSGKKLYAASORAGL 585
 Db 565 KEQLKAYMDPAAFEVKCCAKDDETCFAEBSGKKLYAASORAGL 609

RESULTS 15
 US-10-237-871-2
 Sequence 2, Application US/10237871
 Publication No. US2003036172A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 15
 205 KLDLRLDEGKASSAKURJKCASLQKGERAKWAVARLQSREPKAFATVSKLYVDTK 264
 241 VHECCCHGDLLECADDRADLAKYTCENODSSSKLKECCPKLEKSHCIAEVENDMPA 300
 265 VHECCCHGDLLECADDRADLAKYTCENODSSSKLKECCPKLEKSHCIAEVENDMPA 324
 301 DLSLAADEYPSKDYCKNFAEAADVEGMELYEYARREPKDYSVYLRLAKTYETTLERK 360

Db		325	DLPSLADEFESKDVCKNYAEEKDVTGGMFLYEARFDPDSYVLLRLAKTYTTLIEKC	384
Qy		361	CAAADPHECTAKVFEFPLVVEPQNLIKONCEFEQGEYFQNALLVRYTKVPOYST	420
Db		385	CAAADPHECYAKVFEFPLVVEPQNLIKONCEFEQGEYFQNALLVRYTKVPOYST	444
Qy		421	PTLVEYSRNLGKVGSKCKKHPPEAKRMECAEDYLSVNLNCVILHEKTPYSDRYTKCCES	480
Db		445	PTLVEYSRNLGKVGSKCKKHPPEAKRMECAEDYLSVNLNCVILHEKTPYSDRYTKCCES	504
Qy		481	LYNRPOFSALEYDVTYKPEFNAETTFHADICLSSERERQIKKOTALVELYKHKPAT	540
Db		505	LYNRPOFSALEYDVTYKPEFNAETTFHADICLSSERERQIKKOTALVELYKHKPAT	564
Qy		541	KEQLKAMDDPAAFKCOKADDKETCFAEKGKLVVASQAAIGL	585
Db		565	KEQLKAMDDPAAFKCOKADDKETCFAEKGKLVVASQAAIGL	609

Search completed: August 31, 2003, 16:39:14
 Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2003, 16:33:10 ; Search time 43 seconds
(without alignments)
1308.341 Million cell updates/sec

Title: US-09-833-041-18
Perfect score: 3103
Sequence: 1 DAKKSEVAAHREFKDLGEENFK.....TCAFAEGKLYAASQAAIGL 585

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76-*
1: pir1:
2: pir2:
3: pir3:
4: pir4:
5: abos:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	3103	100.0	609	1	ABHUS		serum albumin prec
2	2942	94.8	600	2	A47591		serum albumin prec
3	2620	84.4	608	2	S57632		serum albumin prec
4	2475	79.8	607	1	ABOS		serum albumin prec
5	2446	78.8	607	1	ABOS		serum albumin prec
6	2432	78.4	607	1	ABSES		serum albumin prec
7	2426	78.2	608	1	ABRVS		serum albumin prec
8	2411	77.7	605	1	ABPGS		serum albumin prec
9	2387	76.9	609	2	JCS538		serum albumin - Mongolia
10	1861	60.0	453	2	A05139		serum albumin - mo
11	1575	50.2	615	1	ABCHS		serum albumin prec
12	1253	40.4	609	2	JC4258		alpha fetoprotein
13	1249	40.3	609	1	FPHU		alpha-fetoprotein
14	1242	40.0	609	1	EPGO		74K albumin precursor
15	1205	38.8	607	1	ABXL72		66K serum albumin
16	1181	38.1	265	2	ABXL68		alpha-fetoprotein
17	1175	37.9	608	1	ABXL68		alpha-fetoprotein
18	1084	34.9	605	1	PPMS		alpha-fetoprotein
19	1067	34.4	611	1	PPMS		alpha-fetoprotein
20	1055	34.0	599	1	A54906		alpha-fetoprotein
21	928.5	29.9	614	2	S59517		alpha-fetoprotein
22	928	29.9	608	2	A53195		alpha-fetoprotein
23	747.5	24.1	608	1	ABON51		serum albumin 1 pr
24	742.5	23.9	608	1	ABON51		serum albumin 2 pr
25	699	22.5	382	2	A37233		serum albumin - bu
26	440.5	14.2	1423	1	S27541		serum albumin - se
27	386	12.4	474	1	VRHOD		vitamin D-binding
28	385	12.4	476	1	VRHOD		vitamin D-binding
29	372	12.0	472	1	A35327		vitamin D-binding

A; Note: this frame-shift variant is designated albumin Bazzano; four additional variants
 B; Menaya, J.; Parrilla, R.; Ayuso, M.S.
 Submitted to the EMBL Data Library, March 1995
 A; Reference number: G08292
 A; Accession: G01747
 A; Status: translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-120, 'G', 122-455 <MEN>
 A; Cross-references: EMBL:U22261; NID:9753428; PMID:6492211; PID:6763431
 R; Ledgerwood, E.C.; George, P.M.; Peck, R.J.; Brennan, S.O.
 Biochem. J. 308, 321-325, 1995
 A; Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast Kex2
 A; Reference number: S55314; PMID:95275251; PMID:775581
 A; Accession: S55314
 A; Molecule type: protein
 A; Residues: 19-27 <LED>
 R; Meloun, B.; Moravek, L.; Kostka, V.
 FEBS Lett. 58, 134-137, 1975
 A; Title: Complete amino acid sequence of human serum albumin.
 A; Reference number: A91420; PMID:76187907; PMID:1225573
 A; Accession: A91420
 A; Molecule type: protein
 A; Residues: 25-171, 'EQ', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-
 R; Roehr, U.; Spittel, G.; Trippel, D.; angstroms
 Justus Liebigs Ann. Chem. 9, 881-884, 1988
 A; Title: Isolation and structure elucidation of middle-molecular weight peptides from ur-
 A; Reference number: S06422
 A; Note: this paper is in German, with an English abstract
 A; Accession: S06422
 A; Molecule type: protein
 A; Residues: 25-48 <ROE>
 R; Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
 Arch. Biochem. Biophys. 305, 595-599, 1993
 A; Title: Mass spectrometric identification of modifications to human serum albumin treat-
 A; Accession: S36882; PMID:93384321; PMID:873198
 A; Molecule type: protein
 A; Residues: 45-67; 141-160; 311-337; 469-490; 570-581 <FIN>
 R; Kausler, E.; Spittel, G.
 Biochim. Hoppe-Seyler 372, 849-855, 1991
 A; Title: Bruchstücke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol-
 A; Reference number: S17599; PMID:92126241; PMID:1772598
 A; Molecule type: protein
 A; Residues: 25-54; 354-357; 431-447 <KAU>
 R; Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
 J. Immunol. 143, 1680-1684, 1989
 A; Title: Structures of histamine-releasing peptides formed by the action of acid proteases
 A; Reference number: A45800; PMID:89341406; PMID:2474609
 A; Accession: A45800
 A; Molecule type: protein
 A; Residues: 166-173 <CAR>
 R; Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; We-
 Biochem. Biophys. Res. Commun. 136, 983-988, 1986
 A; Title: The amino acid sequence of kinetopeptide, a novel peptide isolated from pepsin-tri-
 A; Reference number: A03239; PMID:86242180; PMID:3087552
 A; Accession: A03239
 A; Molecule type: protein
 A; Residues: 166-173 'L' <MOG>
 R; Galliotti, M.; Minchietti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
 A; Title: Mutations in genetic variants of human serum albumin found in Italy.
 A; Reference number: A38255; PMID:91062352; PMID:2247440
 A; Accession: C38255
 A; Molecule type: protein
 A; Residues: 76-111 <GAL1>
 A; Accession: B38255
 A; Molecule type: protein
 A; Residues: 82-105, 'K', 107-110 <GAL2>
 A; Note: this variant is designated albumin Vibo Valentia
 A; Accession: A38255
 A; Molecule type: protein
 A; Residues: 1-120, 'G', 122-455 <MEN>
 A; Cross-references: EMBL:U22261; NID:9753428; PMID:6492211; PID:6763431
 A; Note: this variant is designated albumin Herborn
 R; Minchietti, L.; Galliotti, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Por-
 Biochem. Biophys. Acta 1119, 232-238, 1992
 A; Title: Two alloalbumins with identical electrophoretic mobility are produced by diff-
 A; Reference number: S33298; PMID:9329504; PMID:8513793
 A; Accession: S33298
 A; Molecule type: protein
 A; Residues: 255-263, 'E', 265-281 <MIN1>
 A; Note: this variant is designated albumin Sondrio; another variant Paris-2 is report-
 R; Minchietti, L.; Galliotti, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Por-
 Biochem. Biophys. Acta 1119, 232-238, 1992
 A; Title: Two alloalbumins with identical electrophoretic mobility are produced by diff-
 A; Reference number: S21078; PMID:92190239; PMID:1347703
 A; Accession: S21078
 A; Molecule type: protein
 A; Residues: 354-356, 'K', 358-378 <MIN2>
 A; Note: this variant is designated albumin Sondrio; another variant Paris-2 is report-
 R; Minchietti, L.; Galliotti, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Por-
 Biochem. Biophys. Acta 1119, 232-238, 1992
 A; Title: Atomic structure and chemistry of human serum albumin.
 A; Reference number: A6756; PMID:9233427; PMID:1630489
 A; Contents: annotation; X-ray crystallography, 2.8 angstroms
 R; Brown, J.R.; Shockley, P.; Behrens, P.-O.
 in The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp.23-
 A; Reference number: A94422
 A; Contents: annotation; three-dimensional structure and disulfide bonds
 R; Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
 Collect. Czech. Chem. Commun. 42, 564-579, 1977
 A; Title: Disulfide bonds in human serum albumin.
 A; Reference number: A90930
 R; Jacobson, C.
 Biochem. J. 171, 453-459, 1978
 A; Title: Lysine residue 240 of human serum albumin is involved in high-affinity bind-
 A; Reference number: A90299; PMID:8186630; PMID:656055
 A; Contents: annotation; bilirubin-binding site
 R; Pfters, T.; Reed, R.G.
 in Albumin: Structure, Biosynthesis, Function, Peters, J., and sjoholm, I., eds., 11-
 A; Title: Serum albumin: conformation and active sites.
 A; Reference number: A94408
 A; Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein ge-
 A; Contents: annotation; gene position
 R; Harper, M.E.; Dugaiczky, A.
 Am. J. Hum. Genet. 35, 565-572, 1983
 A; Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein ge-
 A; Contents: annotation; gene position
 R; Walker, J.E.
 FEBS Lett. 66, 173-175, 1976
 A; Title: Lysine residue 199 of human serum albumin is modified by acetylsalicyclic ac-
 A; Reference number: A90028; PMID:33279982; PMID:6192711
 A; Contents: annotation
 A; Note: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicyclic ac-
 a; atase activity
 R; Bohney, J.P.; Ponda, M.L.; Feldhoff, R.C.
 FEBS Lett. 298, 266-268, 1992
 A; Title: Identification of Lys1901 as the primary binding site for pyridoxal 5'-phos-
 A; Reference number: A56294; PMID:92183881; PMID:1544460
 A; Contents: annotation
 A; Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; 1
 C; Comment: serum albumin repeat homology
 C; Keywords: serum albumin; repeat homology
 C; Comment: A large number of variants of human serum albumin have been described.
 C; Genetics:
 A; Gene: GDB:ALB
 A; Cross-references: GDB:118996; OMIM:103600
 A; Map position: 4q11-q13
 C; Superfamily: serum albumin
 C; Comment: serum albumin; duplication; metal binding; phosphoprotein; plasma; pyri-
 doxal; protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (we-
 llirubin).
 F; 19-24/Domain: signal sequence #status predicted <SIG>
 F; 25-60/Domain: propeptide #status experimental <PRO>
 F; 29-202/Domain: serum albumin #status experimental <SA1>

F;166-174/Product: kinetensin #status experimental <KIP>

F;221-394/Domain: serum albumin repeat homology <SA2>

F;27/Binding site: copper (His) #status predicted

F;77-86,99-115,114-125,148-153,192-201,24-210,269-277,289-303,302-313,340-385,384-393,4

F;214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 100.0% ; Score 3103; DB 1; Length 609;
Best Local Similarity 100.0% ; Pred. No. 9.2e-18e;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEYAHRFKDGLGENPKVLAIAQYIQLQCPFEDHVKLYNEVTEFAKTCYADESAE 60

QY 25 DAHKSEYAHRFKDGLGENPKVLAIAQYIQLQCPFEDHVKLYNEVTEFAKTCYADESAE 84

QY 61 NCDKSLHFLFGDKLCTVATLREYNGEMADCAKQPERNECFLQHKDDNPNLPLVPRV 120

QY 85 NCDKSLHFLFGDKLCTVATLREYNGEMADCAKQPERNECFLQHKDDNPNLPLVPRV 144

QY 121 DVMCTAIDNEETFLKLYETIARHRYFYAPELLFFAKRYKAFTCCOADAQCLIP 180

QY 145 DVMCTAIDNEETFLKLYETIARHRYFYAPELLFFAKRYKAFTCCOADAQCLIP 204

QY 181 KLDERDEGKASSAKORLKCASTQKGERAKWAVALSORPKAFAEYSKLYTDLTK 240

QY 205 KLDERDEGKASSAKORLKCASTQKGERAKWAVALSORPKAFAEYSKLYTDLTK 264

QY 241 VHTECCHDLECAADDRAILAKTCENODSISKKLKECCEPKLIEKSHCTAEVENDPA 300

QY 265 VHTECCHDLECAADDRAILAKTCENODSISKKLKECCEPKLIEKSHCTAEVENDPA 324

QY 301 DPLSLAADFVESKDVKCNYTAAKDFVLMGFLYIAYARRHDPDSYVLLRLAKTYETLTKC 360

QY 325 DPLSLAADFVESKDVKCNYTAAKDFVLMGFLYIAYARRHDPDSYVLLRLAKTYETLTKC 384

QY 361 CAAADPHFCYAKVDFEKFPLVEEPONLTKONCELEFOLGEYKTONALVRYTKVQYST 420

QY 361 CAAADPHFCYAKVDFEKFPLVEEPONLTKONCELEFOLGEYKTONALVRYTKVQYST 420

QY 385 CAAADPHFCYAKVDFEKFPLVEEPONLTKONCELEFOLGEYKTONALVRYTKVQYST 444

QY 421 PTLYEVSNLKGWSCKKPEARMPAEDYLSTYVLNOLCVLHEKTPVSDRVTCCTES 480

QY 445 PTLYEVSNLKGWSCKKPEARMPAEDYLSTYVLNOLCVLHEKTPVSDRVTCCTES 504

QY 481 LVNRRPCSALEYDYYVKEPNEETPFADICLTSERERQIKKQPALVELVKHKPKAT 540

QY 505 LVNRRPCSALEYDYYVKEPNEETPFADICLTSERERQIKKQPALVELVKHKPKAT 564

QY 541 KEQLKAVMDDAFVFKCCKADDKETCPAEGEKGKLYASAQALGL 585

QY 565 KEQLKAVMDDAFVFKCCKADDKETCPAEGEKGKLYASAQALGL 609

RESULT 3

S57632 serum albumin precursor - cat

C:Species: Felis silvestris catus (domestic cat)

C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999

C:Accession: A47391

Db 446 PTLYEVSNLKGWSCKKPEARMPAEDYLSTYVLNOLCVLHEKTPVSDRVTCCTES 556

QY 481 LVNRRPCSALEYDYYVKEPNEETPFADICLTSERERQIKKQPALVELVKHKPKAT 583

QY 541 KEQLKAVMDDAFVFKCCKADDKETCPAEGEKGKLYASAQALGL 599

Db 557 KEQLKAVMDDAFVFKCCKADDKETCPAEGEKGKLYASAQALGL 599

RESULT 2

A47391 serum albumin precursor - rhesus macaque

C:Species: Macaca mulatta (rhesus macaque)

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999

R:Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwillet, J.; Putnam, F.

Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993

A;Reference number: A47391; MUID:33211971; PMID:8460152

A;Contents: B/B homozyme

A;Accession: A47391

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-600 <WAT>

A;Cross references: GB:M90463; NID:9342294; PID:AAA36906.1; PMID:9342295

A;Experimental source: liver

A;Cross references: EMBL:X84842; NID:9886484; PID:CAA59279.1; PMID:8647469

A;Molecule type: mRNA

A;Residues: 1-600 <H12>

A;Cross references: EMBL:X84842; NID:9886484; PID:CAA59279.1; PMID:8647469

A;Experimental source: liver

A;Cross references: EMBL:X84842; NID:9886484; PID:CAA59279.1; PMID:8647469

A;Comment: This protein is the major protein component in plasma. It functions as a

ein has 35 conserved cysteine residues.

C:Superfamily: serum albumin repeat homology

C:Keywords: liver; Plasma

F;1-18/Domain: signal sequence #status Predicted <SIG>

F;19-24/Domain: propeptide #status Predicted <PRP>

F;25-608/Product: serum albumin #status Predicted <MAT>

F;29-204/Domain: serum albumin repeat homology <SA1>

F;221-384/Domain: serum albumin repeat homology <SA2>

F;413-592/Domain: serum albumin repeat homology <SA3>

F;405-584/Domain: serum albumin repeat homology <SA3>

Query Match 100.0% ; Score 2942; DB 2; Length 600;

Best Local Similarity 93.5%; Pred. No. 4e-187;

Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 1 DAHKSEYAHRFKDGLGENPKVLAIAQYIQLQCPFEDHVKLYNEVTEFAKTCYADESAE 60

QY 17 DTHKSEYAHRFKDGLGEHFKGLVLVASYLQOCFEEVYKLYNEVTEFAKTCYADESAE 76

Db 61 NCDKSLHFLFGDKLCTVATLREYNGEMADCAKQPERNECFLQHKDDNPNLPLVPRV 120

Db 77 NCDKSLHFLFGDKLCTVATLREYNGEMADCAKQPERNECFLQHKDDNPNLPLVPRV 136

QY 121 DVMCTAIDNEETFLKLYETIARHRYFYAPELLFFAKRYKAFTCCOADAQCLIP 180

Db 137 DVMCTAIDNEETFLKLYETIARHRYFYAPELLFFAKRYKAFTCCOADAQCLIP 196

QY 181 KLDERDEGKASSAKORLKCASTQKGERAKWAVALSORPKAFAEYSKLYTDLTK 240

Db 197 KLDERDEGKASSAKORLKCASTQKGERAKWAVALSORPKAFAEYSKLYTDLTK 256

QY 241 VHTECCHDLECAADDRAILAKTCENODSISKKLKECCEPKLIEKSHCTAEVENDPA 300

Db 257 VHTECCHDLECAADDRAILAKTCENODSISKKLKECCEPKLIEKSHCTAEVENDPA 316

QY 301 DPLSLAADFVESKDVKCNYTAAKDFVLMGFLYIAYARRHDPDSYVLLRLAKTYETLTKC 360

Db 317 DPLSLAADFVESKDVKCNYTAAKDFVLMGFLYIAYARRHDPDSYVLLRLAKTYETLTKC 376

QY 361 CAAADPHFCYAKVDFEKFPLVEEPONLTKONCELEFOLGEYKTONALVRYTKVQYST 420

Db 377 CAAADPHFCYAKVDFEKFPLVEEPONLTKONCELEFOLGEYKTONALVRYTKVQYST 436

QY 421 PTLYEVSNLKGWSCKKPEARMPAEDYLSTYVLNOLCVLHEKTPVSDRVTCCTES 460

Db 437 PTLYEVSNLKGWSCKKPEARMPAEDYLSTYVLNOLCVLHEKTPVSDRVTCCTES 496

QY 481 LVNRRPCSALEYDYYVKEPNEETPFADICLTSERERQIKKQPALVELVKHKPKAT 540

Db 497 LVNRRPCSALEYDYYVKEPNEETPFADICLTSERERQIKKQPALVELVKHKPKAT 556

QY 541 KEQLKAVMDDAFVFKCCKADDKETCPAEGEKGKLYASAQALGL 585

Db 557 KEQLKAVMDDAFVFKCCKADDKETCPAEGEKGKLYASAQALGL 609

RESULT 3

S57632 serum albumin precursor - cat

C:Species: Felis silvestris catus

C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999

C:Accession: A47391

Db 700 PTLYEVSNLKGWSCKKPEARMPAEDYLSTYVLNOLCVLHEKTPVSDRVTCCTES 556

QY 481 LVNRRPCSALEYDYYVKEPNEETPFADICLTSERERQIKKQPALVELVKHKPKAT 583

Db 557 KEQLKAVMDDAFVFKCCKADDKETCPAEGEKGKLYASAQALGL 599

Query	Match 84.4%; Score 2620; DB 2; Length 608;	Query Match 79.8%; Score 2475.5; DB 1; Length 607;
Best Local Similarity 82.0%; Pred. No. 8.2e-166; Matches 478; Conservative 52; Mismatches 53; Indels 0; Gaps 0;	Best Local Similarity 76.3%; Pred. No. 3e-156; Matches 445; Conservative 69; Mismatches 68; Indels 1; Gaps 1;	
Qy 1 DAHKSEVAHFRDGEENFKALVIAFQYIQLQCPFEDHVKLVNEYTEFAKTCVADSAE 60	Qy 1 DAHKSEVAHFRDGEENFKALVIAFQYIQLQCPFEDHVKLVNEYTEFAKTCVADSAE 60	
Db 25 EAHQSEAHFENDGEERFLGVLVAFQSYIQLQCPFEDHVKLVNEYTEFAKCTADQSA 84	Db 25 EAHQSEAHFENDGEERFLGVLVAFQSYIQLQCPFEDHVKLVNEYTEFAKCAADESAE 84	
Qy 61 NCDSLHTLFGDKLCTVATLRETYGMADCCAKOKEPERNECFLQHKDDNPPLPRYREV 120	Qy 61 NCDSLHTLFGDKLCTVATLRETYGMADCCAKOKEPERNECFLQHKDDNPPLPRYREV 120	
Db 85 NCEKSHFLLGDKLCTVASLRKYGNAECDCEKKPERNECFLQHKDDNPPLPRYREV 144	Db 85 NCDSLHTLFGDKLCTVATLRETYGMADCCAKOKEPERNECFLQHKDDNPPLKPLK 143	
Qy 121 DYMCTAHPDNEETFKLYLEIARRHYPYAPELLPEAKRYKAATFCCQAAAKAACLIP 180	Qy 121 DYMCTAHPDNEETFKLYLEIARRHYPYAPELLPEAKRYKAATFCCQAAAKAACLIP 180	
Db 145 DANCTAHPHENQRFQGKLYLEIARRHYPYAPELLPEAKRYKAATFCCQAAAKAACLIP 204	Db 144 DAQCAAFQDPPDKFLGQYLYEVARHYPYGPPELLPEAKYKADTECPADPLKACLIP 203	
Qy 181 KLDLDEGKASSAKORLKCASLQKGERAKVARLISORPKFAEAVSKLYTDLT 240	Qy 181 KLDLDEGKASSAKORLKCASLQKGERAKVARLISORPKFAEAVSKLYTDLT 240	
Db 205 KVDALERKVLAASSERULKCASLQKGERAKVARLISORPKFAEAVSKLYTDLT 264	Db 204 KLDALKERLILSSAKERLKCSSFQNFGRAVANSTARSOKSFPADEFEVSKIVDLT 263	
Qy 241 VHTECCHGDLLECADDRADLAKTYCENODSISTKUECOKPYLEKSHC1AEVENDEMPA 300	Qy 241 VHTECCHGDLLECADDRADLAKTYCENODSISTKUECOKPYLEKSHC1AEVENDEMPA 300	
Db 265 DLPSSLAADFVESKDVKYNTAEEKDVLGMFLYEAARRHDPDSVYLLRLAKTYETTLERK 360	Db 264 VHKECCHGDLLEADDRADLAKTYCENODSISTKUECOKPYLEKSHC1AEVENDEMPA 323	
Qy 301 DLPSSLAADFVESKDVKYNTAEEKDVLGMFLYEAARRHDPDSVYLLRLAKTYETTLERK 360	Qy 301 DLPSLAADFVESKDVKYNTAEEKDVLGMFLYEAARRHDPDSVYLLRLAKTYETTLERK 360	
Db 325 DLPPLAYDFTVEDKEYCKNQEAQDVFLGFTLETSRSHPEYTSVLLRLAKYEATLERC 384	Db 324 DLPSLAADFVESKDVKYNTAEEKDVLGMFLYEAARRHDPDSVYLLRLAKTYETTLERK 383	
Qy 361 CAAADPHECTAYKVFDEFKPLVVEPONLKKONCFLPEQGEYKQNALLVRYTKVPOYST 420	Qy 361 CAAADPHECTAYKVFDEFKPLVVEPONLKKONCFLPEQGEYKQNALLVRYTKVPOYST 420	
Db 385 CAADDPPACAYAHVFDEFKPLVVEPONLKKONCFLPEQGEYKQNALLVRYTKVPOYST 444	Db 384 CAADDPPACAYAHVFDEFKPLVVEPONLKKONCFLPEQGEYKQNALLVRYTKVPOYST 443	
Qy 421 PTLYEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRVTKCCES 480	Qy 421 PTLYEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRVTKCCES 480	
Db 445 PTLYEVSRSLGKVGSCKCCTHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRVTKCCES 504	Db 444 PTLYEVSRNLGKVGSCKCKHPEAKRMPCAEDYLSTVLNOLCVLHEKTPVSDRVTKCCES 503	
Qy 481 LYNRCPFSALEVDFTYKPEKNAEFTFHADICLTSERFQIKQHATVLYKHEKPKAT 540	Qy 481 LYNRCPFSALEVDFTYKPEKNAEFTFHADICLTSERFQIKQHATVLYKHEKPKAT 540	
Db 505 LYNRCPFSAQDVDTYKPEKFAEFTFHADICLTSERFQIKQHATVLYKHEKPKAT 564	Db 504 LYNRCPFSALEDGVYKPEKFAEFTFHADICLTSERFQIKQHATVLYKHEKPKAT 563	
Qy 541 KEQLKAYMDFAAFYEKCCKADDKETCFAAEGKKLIVAAQQAAL 583	Qy 541 KEQLKAYMDFAAFYEKCCKADDKETCFAAEGKKLIVAAQQAAL 583	
Db 565 EQQLKTYWGDGSFYVKDCCAEDKACFAAEFGPKLIVAAQQAAL 607	Db 564 KEQLKTYWGDGSFYVKDCCAEDKACFAAEFGPKLIVAAQQAAL 606	

RESULT 4

ABHOS

serum albumin precursor - horse

C;Species: Equus caballus (domestic horse)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999

C;Reference number: S34053

R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigs, P.D.; Carter, D.C.

C;Superfamily: serum albumin repeat homology

C;Keywords: carrier protein; duplication; metal binding; Plasma

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-24/Domain: propeptide #status predicted <PRO>

F;25-607/Product: serum albumin #status predicted <WAT>

F;29-393/Domain: serum albumin repeat homology <SA1>

F;220-393/Domain: serum albumin repeat homology <SA2>

F;412-591/Domain: serum albumin repeat homology <SA3>

F;27-283/Domain: copper (Hg) #status predicted <PRO>

F;77-863/Domain: bilirubin (Lys) #status predicted

F;263/Binding site: bilirubin (Lys) #status predicted

RESULT 5

ABROS

serum albumin precursor [validated] - bovine

N;Alternate names: 67K protein; preproalbumin

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000

C;Accession: A38885; A36401; A30780; S10808; B645800; A66693; A90309; A91458;

R;Holowachuk, E.W.; Stoltzberg, J.K.; Reed, R.G.; Peters, Jr., T.

C;Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27 nm

A;Reference number: S34053; MUID:93345495; PMID:8344282

A;Accession: S34053

A;Molecule type: mRNA

A;Residues: 1-607 <H0A>

A;Cross-references: GB:XY74045; NID:9399671; PID:9399672

C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membra

C;Superfamily: serum albumin repeat homology

C;Keywords: carrier protein; duplication; metal binding; Plasma

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-24/Domain: propeptide #status predicted <PRO>

F;25-607/Product: serum albumin #status predicted <WAT>

F;29-393/Domain: serum albumin repeat homology <SA1>

F;220-393/Domain: serum albumin repeat homology <SA2>

F;412-591/Domain: serum albumin repeat homology <SA3>

F;27-283/Domain: copper (Hg) #status predicted <PRO>

F;77-863/Domain: bilirubin (Lys) #status predicted

F;263/Binding site: bilirubin (Lys) #status predicted

A;Molecule type: protein

A;Accession: A91258

A;Reference number: A91258; PMID:80024278; PMID:488109

QY	442	TIVVEBRNLGKVSKCKXPKRMPAEDYLSTVNLQCVLHEKTVSDRVTKCCTEIL	481	495	ETYVPKEFNAETTFHADICTSEKERQIKKQT	527
Db	447	TIVVEARSLGVRGTHCCLPKRMPAEDYLSTVNLQCVLHEKTVSDRVTKCCTGGL	506	521	ETYVPKEFNAETTFHSDICTLPEKEKIKKQT	453
QY	482	VNRPGESALEDFTYKPEKEFNAETTFHADICTLSEKERQIKKQTALVELYKPKATK	541			
Db	507	VERRPGESALPDYDFTYKPEKEFNAETTFHADICTLPEKEKOMERKPAEALVELYKPKQATE	566	547	RESULT 11	
QY	542	EQLKAVDDEAFAFVEKCKDADKETTAEAGKLVAAASAAAL	583	570	serum albumin precursor - chicken	
Db	567	EQLKXWGMGDEAEEFKCKQKEAESTGPKLVAAESOKAL	608	571	C;Species: Gallus gallus (chicken)	
QY	581	: : : : : : : : :	628	572	C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999	
Db	582	: : : : : : : : :	629	573	C;Accession: SL15571; A05078; AL18737	
QY	583	: : : : : : : : :	630	574	R;Cassady, A. I.; Salkild, C. K.; Baverstock, P.; Wallace, J. C.	
Db	584	: : : : : : : : :	631	575	R;Submitted to the EMBL Data Library, July 1991	
QY	585	: : : : : : : : :	632	576	A;Reference number: A05139; MUID:815571; PMID:618737	
Db	586	: : : : : : : : :	633	577	A;Accession: A05139	
QY	587	: : : : : : : : :	634	578	A;Molecule type: mRNA	
Db	588	: : : : : : : : :	635	579	A;Molecule type: DNA	
QY	589	: : : : : : : : :	636	580	A;Residues: 1-615 <CAS>	
Db	590	: : : : : : : : :	637	581	A;Cross-references: EMBL: X60688; PIDN:CAA43098; PIDN:CAA23680; PIDN:963038; PIDN:963039	
QY	591	: : : : : : : : :	638	582	R;Rosen, A. M.; Geller, D. M.	
Db	592	: : : : : : : : :	639	583	R;Hache, R. J. G.; Wiskocil, R.; Yisa, M.; Roy, R. N.; Lau, P. C. K.; Deesley, R. G.	
QY	593	: : : : : : : : :	640	584	R;Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977	
Db	594	: : : : : : : : :	641	585	A;Title: Chicken microsomal albumin: amino terminal sequence of chicken prealbumin.	
QY	595	: : : : : : : : :	642	586	A;Title: the 5', noncoding and flanking regions of the avian very low density apolipoprotein A;Reference number: A05078; MUID:81361037; PMID:81361037	
Db	596	: : : : : : : : :	643	587	A;Accession: A05078	
QY	597	: : : : : : : : :	644	588	A;Accession: A05139	
Db	598	: : : : : : : : :	645	589	A;Accession: A05139	
QY	599	: : : : : : : : :	646	590	A;Accession: A05139	
Db	600	: : : : : : : : :	647	591	A;Accession: A05139	
QY	601	: : : : : : : : :	648	592	A;Accession: A05139	
Db	602	: : : : : : : : :	649	593	A;Accession: A05139	
QY	603	: : : : : : : : :	650	594	A;Accession: A05139	
Db	604	: : : : : : : : :	651	595	A;Accession: A05139	
QY	605	: : : : : : : : :	652	596	A;Accession: A05139	
Db	606	: : : : : : : : :	653	597	A;Accession: A05139	
QY	607	: : : : : : : : :	654	598	A;Accession: A05139	
Db	608	: : : : : : : : :	655	599	A;Accession: A05139	
QY	609	: : : : : : : : :	656	600	A;Accession: A05139	
Db	610	: : : : : : : : :	657	601	A;Accession: A05139	
QY	611	: : : : : : : : :	658	602	A;Accession: A05139	
Db	612	: : : : : : : : :	659	603	A;Accession: A05139	
QY	613	: : : : : : : : :	660	604	A;Accession: A05139	
Db	614	: : : : : : : : :	661	605	A;Accession: A05139	
QY	615	: : : : : : : : :	662	606	A;Accession: A05139	
Db	616	: : : : : : : : :	663	607	A;Accession: A05139	
QY	617	: : : : : : : : :	664	608	A;Accession: A05139	
Db	618	: : : : : : : : :	665	609	A;Accession: A05139	
QY	619	: : : : : : : : :	666	610	A;Accession: A05139	
Db	620	: : : : : : : : :	667	611	A;Accession: A05139	
QY	621	: : : : : : : : :	668	612	A;Accession: A05139	
Db	622	: : : : : : : : :	669	613	A;Accession: A05139	
QY	623	: : : : : : : : :	670	614	A;Accession: A05139	
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QY	625	: : : : : : : : :	672	616	A;Accession: A05139	
Db	626	: : : : : : : : :	673	617	A;Accession: A05139	
QY	627	: : : : : : : : :	674	618	A;Accession: A05139	
Db	628	: : : : : : : : :	675	619	A;Accession: A05139	
QY	629	: : : : : : : : :	676	620	A;Accession: A05139	
Db	630	: : : : : : : : :	677	621	A;Accession: A05139	
QY	631	: : : : : : : : :	678	622	A;Accession: A05139	
Db	632	: : : : : : : : :	679	623	A;Accession: A05139	
QY	633	: : : : : : : : :	680	624	A;Accession: A05139	
Db	634	: : : : : : : : :	681	625	A;Accession: A05139	
QY	635	: : : : : : : : :	682	626	A;Accession: A05139	
Db	636	: : : : : : : : :	683	627	A;Accession: A05139	
QY	637	: : : : : : : : :	684	628	A;Accession: A05139	
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Db	640	: : : : : : : : :	687	631	A;Accession: A05139	
QY	641	: : : : : : : : :	688	632	A;Accession: A05139	
Db	642	: : : : : : : : :	689	633	A;Accession: A05139	
QY	643	: : : : : : : : :	690	634	A;Accession: A05139	
Db	644	: : : : : : : : :	691	635	A;Accession: A05139	
QY	645	: : : : : : : : :	692	636	A;Accession: A05139	
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QY	647	: : : : : : : : :	694	638	A;Accession: A05139	
Db	648	: : : : : : : : :	695	639	A;Accession: A05139	
QY	649	: : : : : : : : :	696	640	A;Accession: A05139	
Db	650	: : : : : : : : :	697	641	A;Accession: A05139	
QY	651	: : : : : : : : :	698	642	A;Accession: A05139	
Db	652	: : : : : : : : :	699	643	A;Accession: A05139	
QY	653	: : : : : : : : :	700	644	A;Accession: A05139	
Db	654	: : : : : : : : :	701	645	A;Accession: A05139	
QY	655	: : : : : : : : :	702	646	A;Accession: A05139	
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QY	657	: : : : : : : : :	704	648	A;Accession: A05139	
Db	658	: : : : : : : : :	705	649	A;Accession: A05139	
QY	659	: : : : : : : : :	706	650	A;Accession: A05139	
Db	660	: : : : : : : : :	707	651	A;Accession: A05139	
QY	661	: : : : : : : : :	708	652	A;Accession: A05139	
Db	662	: : : : : : : : :	709	653	A;Accession: A05139	
QY	663	: : : : : : : : :	710	654	A;Accession: A05139	
Db	664	: : : : : : : : :	711	655	A;Accession: A05139	
QY	665	: : : : : : : : :	712	656	A;Accession: A05139	
Db	666	: : : : : : : : :	713	657	A;Accession: A05139	
QY	667	: : : : : : : : :	714	658	A;Accession: A05139	
Db	668	: : : : : : : : :	715	659	A;Accession: A05139	
QY	669	: : : : : : : : :	716	660	A;Accession: A05139	
Db	670	: : : : : : : : :	717	661	A;Accession: A05139	
QY	671	: : : : : : : : :	718	662	A;Accession: A05139	
Db	672	: : : : : : : : :	719	663	A;Accession: A05139	
QY	673	: : : : : : : : :	720	664	A;Accession: A05139	
Db	674	: : : : : : : : :	721	665	A;Accession: A05139	
QY	675	: : : : : : : : :	722	666	A;Accession: A05139	
Db	676	: : : : : : : : :	723	667	A;Accession: A05139	
QY	677	: : : : : : : : :	724	668	A;Accession: A05139	
Db	678	: : : : : : : : :	725	669	A;Accession: A05139	
QY	679	: : : : : : : : :	726	670	A;Accession: A05139	
Db	680	: : : : : : : : :	727	671	A;Accession: A05139	
QY	681	: : : : : : : : :	728	672	A;Accession: A05139	
Db	682	: : : : : : : : :	729	673	A;Accession: A05139	
QY	683	: : : : : : : : :	730	674	A;Accession: A05139	
Db	684	: : : : : : : : :	731	675	A;Accession: A05139	
QY	685	: : : : : : : : :	732	676	A;Accession: A05139	
Db	686	: : : : : : : : :	733	677	A;Accession: A05139	
QY	687	: : : : : : : : :	734	678	A;Accession: A05139	
Db	688	: : : : : : : : :	735	679	A;Accession: A05139	
QY	689	: : : : : : : : :	736	680	A;Accession: A05139	
Db	690	: : : : : : : : :	737	681	A;Accession: A05139	
QY	691	: : : : : : : : :	738	682	A;Accession: A05139	
Db	692	: : : : : : : : :	739	683	A;Accession: A05139	
QY	693	: : : : : : : : :	740	684	A;Accession: A05139	
Db	694	: : : : : : : : :	741	685	A;Accession: A05139	
QY	695	: : : : : : : : :	742	686	A;Accession: A05139	
Db	696	: : : : : : : : :	743	687	A;Accession: A05139	
QY	697	: : : : : : : : :	744	688	A;Accession: A05139	
Db	698	: : : : : : : : :	745	689	A;Accession: A05139	
QY	699	: : : : : : : : :	746	690	A;Accession: A05139	
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QY	701	: : : : : : : : :	748	692	A;Accession: A05139	
Db	702	: : : : : : : : :	749	693	A;Accession: A05139	
QY	703	: : : : : : : : :	750	694	A;Accession: A05139	
Db	704	: : : : : : : : :	751	695	A;Accession: A05139	
QY	705	: : : : : : : : :	752	696	A;Accession: A05139	
Db	706	: : : : : : : : :	753	697	A;Accession: A05139	
QY	707	: : : : : : : : :	754	698	A;Accession: A05139	
Db	708	: : : : : : : : :	755	699	A;Accession: A05139	
QY	709	: : : : : : : : :	756	700	A;Accession: A05139	
Db	710</td					

Db	330	IPLSVERKTYEDKEYCKSFEAGHDAFMAEFVYEYSRHRPEFSIQLIMRATAKGYESLLEKCC	389	Db	321	ERPEGLSPNLNRFLCDRDENQFSSGENKNTILASPTVHESSRRIPOLAVSVILRVAKGYQEL	380	
QY	362	ARADPFECAKVFPEFLPVLVEDPQNLKONCEDEFQGEYEFQNLALVYRKTAKPQSTP	421	QY	357	LERCCARADPHECYAKVFDEFKPLVPERPONLKKONCEFEOLGEYFKFQNLALVYRKTAKP	416	
Db	390	KUDNPNECYANAQEQLQHQLKETDQVKNCDLHLHGEAFLKLSTLTYTKAMPQPTD	449	Db	381	LERCFQPNPFLCQDKGEPELQYIQSQALAKRSCGGFQKQGEYFLQNALPLVAKTAKP	440	
QY	422	TIVYEYSRNLGKVGSKCCKHPEAKRKAFCADYLSVNLQCLVHLKHTPVSDRTKCCESL	481	QY	417	QVSTPTIYEYSRNLGKVGSKCCKHPEAKRKAFCADYLSVNLQCLVHLKHTPVSDRTKIC	476	
Db	450	LLLETPKRMVTTGKCCGCOLGDRRACSGSLSLTVIHDTCRQETPKPTDINVSQCCQLY	509	Db	441	QIHSSELMATRKMMATAATCCOLSEKLLACGSAADTIGHLCRTEPTPNFGYGC	500	
QY	482	VNRPQCSALEVDVTTYKPEKETAEFTFHADICLSEKEROTKQTAVALYELVHKPATK	541	QY	477	CTESLIVNRPRPESALEVDETYKPEKNAEFTFHADICLSEKEROTKQTAVALYELVHK	536	
Db	510	ANRRCPECTANGVDKDVKYVPPPFQDMSFDEKLCSAPABEREGQMLLNLIRKPONTE	569	Db	501	CTSYAAARRPQFSSLVDTDTYVPPAFSDKPLFHKDLCQAGYALQTMKQDEFILNLVQK	560	
QY	542	EQKAYAMDDAFAFVKCOKADDKETPEAEKGKLVIAASQANIGL	585	QY	537	PRATKEQIKAIVMDPFAFVKCOKADDKETPEAEKGKLVIAASQANIGL	585	
Db	570	EQIKTIADGFTAMTDKCKQSDINTCFGEGANLIVQSRATLGI	613	Db	561	PQITEQLEAVIADPSGLEKCCQGQEVCFAEQKLISKTRAAIGV	609	
RESULT 12								
JC4258		alpha-fetoprotein precursor - chimpanzee						
C;Species:	Pan troglodytes (chimpanzee)							
C;Date:	27-Nov-1995	#sequence_revision	08-Feb-1996	#text_change	20-Aug-1999			
C;Accession:	JC4258							
R;Nishio, R.; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczyk, A.								
Gene 162, 213-220, 1995								
A;Title:	The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to t							
A;Reference:	JC4258;							
A;Accession:	JC4258							
A;Molecule type:	DNA							
A;Residues:	1-609 <NLS>							
A;Cross-references:	GB:021916; PIDN:AAA91641.1; PMID:9841312							
C;Comment:	This protein is a plasma protein produced in the fetal and neonatal liver and o							
C;Similarities:	similar properties and structure.							
C;Genetics:								
A;Gene:	afp							
A;Map position:	3P							
A;Introns:	28/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551							
C;ProteinFamily:	serum albumin; serum albumin repeat homology							
C;Keywords:	glycoprotein							
F;1-19/Domain:	signal sequence #status predicted <STIG>							
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F;29-20/2/Domain:	serum albumin repeat homology <SA1>							
F;221-3394/Domain:	serum albumin repeat homology <SA2>							
F;413-592/Domain:	serum albumin repeat homology <SA3>							
F;42,251/Binding site:	carbohydrate (Asn) (covalent) #status predicted							
Query Match	40.4%							
Best Local Similarity	40.4%							
Matches 236;	Conservative 115; Mismatches 231; Indels 7; Gaps 3;							
QY	3 HKSE----VAFRKDLGEGENPKALVIAFQQLQQCPEFDHYKLYNEVTEFAKTCVADE	57	QY	3 HKSE----VAFRKDLGEGENPKALVIAFQQLQQCPEFDHYKLYNEVTEFAKTCVADE	57	QY	3 HKSE----VAFRKDLGEGENPKALVIAFQQLQQCPEFDHYKLYNEVTEFAKTCVADE	57
Db	22 HRNEYGIASLTDSTCCTAHLNLDLATLIEFFQFQEAYKEYSKMVKDALTAIEKPTCDE	81	Db	22 HRNEYGIASLTDSTCCTAHLNLDLATLIEFFQFQEAYKEYSKMVKDALTAIEKPTCDE	81	Db	22 HRNEYGIASLTDSTCCTAHLNLDLATLIEFFQFQEAYKEYSKMVKDALTAIEKPTCDE	81
QY	58 SAENCDLSLHTLFDGKLCVATLRETYGEMADCCAKQEPERNBCFCQHQKDDNP-NLPRIV	116	QY	58 SAENCDLSLHTLFDGKLCVATLRETYGEMADCCAKQEPERNBCFCQHQKDDNP-NLPRIV	116	QY	58 SAENCDLSLHTLFDGKLCVATLRETYGEMADCCAKQEPERNBCFCQHQKDDNP-NLPRIV	116
Db	82 QSGCLENOLPQAFLEKREKELEYGH--SDCCSOSERGRNCNPKLAHKKPTPASIPFQ	140	Db	82 QSGCLENOLPQAFLEKREKELEYGH--SDCCSOSERGRNCNPKLAHKKPTPASIPFQ	140	Db	82 QSGCLENOLPQAFLEKREKELEYGH--SDCCSOSERGRNCNPKLAHKKPTPASIPFQ	140
QY	117 RPEDVYMCATAFHNDPTEFLKLYTLEIARRHYPYFAPELLEFARRKTAFFCQADKRA	176	QY	117 RPEDVYMCATAFHNDPTEFLKLYTLEIARRHYPYFAPELLEFARRKTAFFCQADKRA	176	QY	117 RPEDVYMCATAFHNDPTEFLKLYTLEIARRHYPYFAPELLEFARRKTAFFCQADKRA	176
Db	141 VPEPVTCSEAEEDETFANKFTEYLARRHFLYPTILLWAARYKLIPSCCKRAENAVE	200	Db	141 VPEPVTCSEAEEDETFANKFTEYLARRHFLYPTILLWAARYKLIPSCCKRAENAVE	200	Db	141 VPEPVTCSEAEEDETFANKFTEYLARRHFLYPTILLWAARYKLIPSCCKRAENAVE	200
QY	177 CLPKLDELRLDEGGKASSAKORLKAQSLQKGERAFKAWAVARLQSRPKKAFFAIVSKLYT	236	QY	177 CLPKLDELRLDEGGKASSAKORLKAQSLQKGERAFKAWAVARLQSRPKKAFFAIVSKLYT	236	QY	177 CLPKLDELRLDEGGKASSAKORLKAQSLQKGERAFKAWAVARLQSRPKKAFFAIVSKLYT	236
Db	201 CFQTKAAATVTRKELRESSLNQHACAYAKNFSRTTQALTYTKLQSKETKNTFLQKLYL	260	Db	201 CFQTKAAATVTRKELRESSLNQHACAYAKNFSRTTQALTYTKLQSKETKNTFLQKLYL	260	Db	201 CFQTKAAATVTRKELRESSLNQHACAYAKNFSRTTQALTYTKLQSKETKNTFLQKLYL	260
QY	237 DLKVKHEPCCGDLLECADRADIAYKTCIQNDS5SSKLUKECCPKLEKSHCIAEVEND	296	QY	237 DLKVKHEPCCGDLLECADRADIAYKTCIQNDS5SSKLUKECCPKLEKSHCIAEVEND	296	QY	237 DLKVKHEPCCGDLLECADRADIAYKTCIQNDS5SSKLUKECCPKLEKSHCIAEVEND	296
Db	261 DVAVHHECRCGQDVLCDLQGEKIMSTICSOQDTSNKTCECKLTLERQCIHAAEND	320	Db	261 DVAVHHECRCGQDVLCDLQGEKIMSTICSOQDTSNKTCECKLTLERQCIHAAEND	320	Db	261 DVAVHHECRCGQDVLCDLQGEKIMSTICSOQDTSNKTCECKLTLERQCIHAAEND	320
QY	297 EMPADLPSLAADFESKDVCKNAYAARDVFLGMLFEYARRHEDPSVYLLRLAKTYENT	356	QY	297 EMPADLPSLAADFESKDVCKNAYAARDVFLGMLFEYARRHEDPSVYLLRLAKTYENT	356	QY	297 EMPADLPSLAADFESKDVCKNAYAARDVFLGMLFEYARRHEDPSVYLLRLAKTYENT	356

A;Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609 <TEC>	DB
R;Aoyagi, S.; Hsu, R.; Heinrikson, R.L.; Miller, J.B.	QY
Biochim. Biophys. Acta 493, 418-428, 1977	177 CILEKIDLEDEGKASSAKORLKASLOKEGRAFKAWAYARISORFKAFPAEVSKIVT 236
A;Title: Studies on human alpha-fetoprotein. Isolation and characterization of monomeric	201 CFQTKAAFTVTKLRESSLNQHACAVMNFGRFTQATYTKLSQFETKVNTEIQLVL 260
A;Accession number: A90624; MUID:77242506; PMID:70228	237 DLTKVHTECGBDILCEADRADLAKYCENDSISSKKLECCPKLKSCTIAVEND 296
A;Molecule type: protein	261 DVATVHECGRDVLQDGEKMSYICSQDPLTKTERRGCLTTERGCLTIAEND 320
A;Residues: S',20-22, S',24-35 <YAC>	297 EMPADLPLAADFVSKDVKNTAAKDVYFELMFLYRHPDSYVLLRLAKYET 356
R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.	321 EKPGSPLSPNLLNRLGDDPNTFQFSSGEKNTFLASFVHYSRHPQLAVSTLRYAKQEL 380
Cancer Res. 37, 3661-3667, 1977	357 LEKCGAAADPHECYAKVEDDFKPLVPEPONLIKONGCFLFOLGYKEFONALVYRTKKVP 416
A;Title: Comparative chemical structure of human alpha-fetoproteins from fetal serum and	381 LEKCPQTENPLBQDKGEELQKTYIQESCALAKRSCLGFLQRGEYVLYNALFVATYKAP 440
A;Reference number: A90757; MUID:78001760; PMID:71198	417 QVSPPTLVEVSRLNKGVSCKKPEAKRMPGAEDLSTVYLNQCLVLEKTPVSDRYTKC 476
A;Molecule type: protein	441 QLTSEMAITRMTAATCCQSLSEDILLAGEADDTIGHICRUMTVPNGVQC 500
A;Residues: 'S',20-30, 'A',32-37, 'A' <AOY>	477 CTESLNVRPCPSALEVDEHYVPKFNEFNETFPHADICLISEKEROIKKOTALVELVYHK 536
R;Sakai, M.; Morinata, T.; Urano, Y.; Watanabe, K.; Wegmann, T.G.; Tamada, K.	501 CTSSYANVRPCFSSLYVDEYVPPAFSDKFLFKHQLCQGVALQTKQEFILNLYKQK 560
J. Biol. Chem. 260, 5055-5060, 1985	537 PKATKEQLKAVMDFAFVERKCCADDEKTCFAEGRKLYAASQALG 585
A;Title: The human alpha-fetoprotein gene. Sequence organization and the 5' flanking region	561 PQTPEEQLAEVIAFDSGLEKCCQGQEVCFAEEGQKLISKTRALGY 609
A;Reference number: A92520; MUID:2580830	
A;Contents: annotation; gene; exons and introns	
R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.	
Cancer Res. 38, 3483-3486, 1978	
A;Title: Copper(II)-binding of human alpha-fetoprotein.	
A;Reference number: A90758; MUID:79001617; PMID:80265	
A;Contents: annotation; metal binding	
R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.	
Cancer Res. 39, 3571-3574, 1979	
A;Title: alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding ability	
A;Reference number: A90759; MUID:80001700; PMID:89900	
A;Contents: annotation; bilirubin binding	
C;Comment: AFP is synthesized by the fetal liver and yolk sac. It occurs in the plasma of	
O; trace amounts after birth. The serum level in adults is usually less than 40 ng/ml. At	
C;Comment: Human AFP binds copper, nickel, and fatty acids as well as, and the bilirubin	
properties.	
C;Genetics:	
A;Gene: GDB:AFP	
A;Cross references: GDB:119660; OMIM:104150	
A;Map position: 4q11-4q13	
A;Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551	
C;Superfamily: serum albumin; serum albumin repeat homology	
C;Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma	
F;1-18/Domain: signal sequence #status predicted <SIC>	
F;19-609/Product: alpha-fetoprotein #status experimental <NAT>	
F;20-609/Domain: serum albumin repeat homology <SA1>	
F;221-319/Domain: serum albumin repeat homology <SA2>	
F;222-592/Domain: serum albumin repeat homology <SA3>	
F;224/Binding site: copper (His) #status predicted	
F;99-114;113-124;148-193;192-201;224-270;269-303;302-313;384-393;416-462;472	
F;249/Binding site: bilirubin (Lys) #status predicted	
F;251/Binding site: carbohydrate (Asn) (covalent) #status predicted	
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Best Local Similarity 39.9%; Pred. No. 3.8e-75; Indels 7; Gaps 3;	
Matches 235; Conservative 116; Mismatches 231; Indels 117; Gaps 7; Gaps 3;	
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Db 22 HRNEYGTASLDSQCTAETISLADLTFIAQFQYEAQTKYKEYSKMVDALTAIEKPTGDE 81	22 HRNEYGTASLDSQCTAETISLADLTFIAQFQYEAQTKYKEYSKMVDALTAIEKPTGDE 81
QY 58 SAENCDKSLHTLFGDKLCTVATIREYGENEADCCAKOERPERNECFLQHKDDNP-NLPLV 116	58 SAENCDKSLHTLFGDKLCTVATIREYGENEADCCAKOERPERNECFLQHKDDNP-NLPLV 116
Db 82 QSGGCLENQLPALFELCEKELELKGY-SDCCSQSEEGRMCFLAKKPTPSLIPDQ 140	82 QSGGCLENQLPALFELCEKELELKGY-SDCCSQSEEGRMCFLAKKPTPSLIPDQ 140
QY 117 RPEVDYMCATAFDNDNEETFLKLYLEIARRHPPYFAPELLFFAKRECCQAADKA 176	117 RPEVDYMCATAFDNDNEETFLKLYLEIARRHPPYFAPELLFFAKRECCQAADKA 176

Db	141	VPPEPTSCAYEEDRETMKFIYETARRHFLYPTAPTILLWAARYKIPSCCKRAENAVE	200	F; 25-607/Product: 74K serum albumin #status predicted <MAT> F; 322-301/Domain: serum albumin repeat homology <SA2> F; 3220-393/Domain: serum albumin repeat homology <SA2>
QY	177	CLPKLDELDREGKASSAKQKRCASLQKGERAKWAVALSOPRPAFAEVSKLVFT	236	F; 412-591/Domain: serum albumin repeat homology <SA2>
Db	201	CFQTKAAATVKEKTLQFACATMKNGTFRQATVKEKTLQFETKVNFIQKLVF	260	F; 30/Binding site: copper (His) #status predicted F; 80-98/101-117/116-127,147-192,191-200,223-269/268-276,288-302,301-312,339-384,383- F; 256/Binding site: carbohydrate (Asn) #status predicted
QY	237	DTKTYHTECCGHDILECADDRAKVICENQDTSKLIKECEKTLKSHCTADEVEND	296	
Db	261	DYAHVHEEHCORGDLDCQDGKTMYSICQQDTLSNKITECKLTILERGQCIHAAAND	320	Query Match 38.8%; Score 1205; DB 1; Length 607; Best Local Similarity 39.3%; Pred. No. 3, 3e-7; Matches 227; Conservative 10; Mismatches 239; Indels 4; Gaps 2;
QY	297	EMPADPLSLAADFVEKSKDVKRNAYAARDVFLGMPFLYETARRHFDYSVVLRLAKTYETT	356	
Db	321	ERPEGLSPNLNRFLGDRDENFSSGERNIFLASEVHEYSSRHPQLAVSVILRVAKGYDEL	380	
QY	357	LEKCCAAADPHECAKVDDEFPLVPEPQNLKQNCFLFQIGEYFQNALLVRYTKV	416	QY 3 HKSEYAHFRKDGEENFKALVLLAFAQYLQOCPPFEDBVKLYNETEFAKTYCDAESEN C 62
Db	381	LEKCFQTNPELQCDQKGEELQYKIQSYOALAKRSGLFQKLGEYTTQNLVAYTKKAP	440	Db 30 HHKHAIDVYATLTEREKGTULATVSYQNLQKQSLEUUSKLYNEINDEPKSCINDKPE-C 88
QY	417	QVSTPLVNEVRNQKGVSKCCKHPEAKRPAQAEYDLSVNLQOCYLTQHETPLVSDRTYTKC	476	QY 63 DKSUHFLGDKLQTCVLTRETYGMADCCKAOPERNECFLQHKDDNNLNPRLVREDEV D 122
Db	441	QITSSSEMLAIRTKAATAATACQOLSEDKLLAGCAGGAIDTIGHICRHETMPVPGVQC	500	Db 89 EKPGTLEFDKLCADAVGTYNERSKECAKOPERAQCTKAHDHEH - SKEPEE 145
QY	477	CPELSVYNRPQSALEYDETTYKPEKNAETPTFHADICLTSEKEROIKKOTALYVHK	536	QY 123 MCTAHDNEETFLKLYTETARRHFLYTAPELLEFAKRYKAATTECCQAAQCLPLKL 182
Db	501	CRPSYANRPQFSSLVVDETTYVPPASDDKFLHDKLQAOAQVYALQMKQBEFLINVRQK	560	Db 146 TCKLKEIPDDLISAFTHEBARNHNPDLPPAVIALTRQYKLAHBCBEDKEKCSER M 205
QY	537	PRATKEQKAWMDFAAFAVEKCKADDKETCOPAEGKLVVASOQAGL	585	QY 183 DELRECKASSAKQKRCASLQKGERAKWAVALSOPRKAFAEVSKLYTDLK V 242
Db	561	PQITEEOLFTVIAFSGLEKCCQGQEVEQCFAAEQGQKLISKTRTAALGV	609	Db 206 KOLMKOSISTEKOHFCWLLDNPFKVKLAKNLYSHYPAKFKLAHNFTEEVTHF I 265
QY	592	ABX172	74K albumin precursor - African clawed frog	Db 243 TECCGDLLECAADDRLAKYICQNDSISKLIKECOPPLERSHCIAEVENDEPADL 302
Db	593	ABX172	C;Species: Xenopus laevis (African clawed frog)	Db 266 KDCCHDDMFECMTERLELTHTCQHDKDESSKLEKCONPLLERTYCITYLNDYPAL 325
QY	594	ABX172	C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999	QY 303 PSLAADFVEKSKDVKRNAYAARDVFLGMPFLYETARRHFDYSVVLRLAKTYETTLEKCA 362
Db	595	ABX172	C;Accession: B41682; S0293; A05288	Db 326 SQPTTEFDPHCEYTAENNEVFLGRTLYHAYSRKGELSQQFLQSAKEYTSLNNCK C 385
QY	596	ABX172	R; Moskaitis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R.	QY 363 AADPHECYAKVDFEKFPLVPEPQNLKQNCFLFQIGEYFQNALLVRYTKVPOYSTPT 422
Db	597	ABX172	Mol. Endocrinol. 3, 464-473, 1989	Db 386 TDNPPECYKGDADRENEAKERAYKONCDLHLERGKELNLLRTKMPQYSDET 445
QY	598	ABX172	A;Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic acid during development	QY 423 LVEVSRLGKVGSKCKHPEAKPACEDYLSVNLQCLVHLERKTPVSDRVKCCPESLV 482
Db	599	ABX172	A;Reference number: S02632; PMID:88112470; PMID:1451026	Db 446 LIGIAHONADIGEHCACAVPENORPACEDLTLLGKMCBQKKTFINNHVACCDSYS 505
QY	600	ABX172	A;Accession: B41682	QY 483 NRRPQSALEYDETTYKPEKNAETPTFHADICLTSEKEROIKKOTALYVHKPKATK E 542
Db	601	ABX172	A;Molecule type: mRNA	Db 506 GMRSQFTALGDPDYYPPPTDDFHDKCTANDREKOHKOKFLYKLIVKSPKLEK N 565
QY	602	ABX172	A;Cross-references: EMBL:Z226826	QY 543 QLKAVMDPDAAFPEKCKADDKETCFAEGKLVYASQ 580
Db	603	ABX172	R;Wolffe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, J.L.; Tata, J.	Db 566 HIDRCSAELPKVQCTADHPOPFDTKPVILIERQ 603
QY	604	ABX172	R; Schorpp, M.; Doebbing, U.; Wagner, U.; Ryffel, G.U.	
Db	605	ABX172	J. Mol. Biol. 199, 83-93, 1988	
QY	606	ABX172	A;Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. Dele	
Db	607	ABX172	A;Reference number: S02632; PMID:88112470; PMID:1451026	
QY	608	ABX172	A;Accession: S02632	
Db	609	ABX172	A;Statistical significance: not compared with conceptual translation	
QY	610	ABX172	A;Molecule type: DNA	
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QY	612	ABX172	A;Cross-references: EMBL:Z226826	
Db	613	ABX172	R;Wolffe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, J.L.; Tata, J.	
QY	614	ABX172	R; Schorpp, M.; Doebbing, U.; Wagner, U.; Ryffel, G.U.	
Db	615	ABX172	J. Mol. Biol. 199, 83-93, 1988	
QY	616	ABX172	A;Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and destabilization	
Db	617	ABX172	A;Reference number: A05288; PMID:85126974; PMID:3971963	
QY	618	ABX172	A;Accession: A05288	
Db	619	ABX172	A;Molecule type: mRNA	
QY	620	ABX172	A;Residues: 45-502, L', 504-557 <WOL>	
Db	621	ABX172	A;Cross-references: GB:M28276	
QY	622	ABX172	A;Note: the authors translated the codon TAT for residue 63 as thr	
Db	623	ABX172	C;Comment: Serum albumin is synthesized in the liver as prealbumin. It binds copper, mones (weak bonds with these hormones promote their transfer across the membranes), thy	
QY	624	ABX172	C;Genetics: A;Introns: 27/1	
Db	625	ABX172	C;Superfamily: serum albumin repeat homology	
QY	626	ABX172	C;Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma	
Db	627	ABX172	F; 1-18/Domain: signal sequence #status Predicted <SIG>	
QY	628	ABX172	F; 19-24/Domain: Propeptide #status Predicted <PRO>	

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Job time : 45 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.						
on: August 31, 2003, 16:33:10 ; Search time 25 Seconds (without alignments) 1100.425 Million cell updates /						
title: US-09-833-041-18						
perfect score: 3103						
sequence: 1 DAHKSEYAHRFKDLGGENFK.....TCFAEFGKLVYAAQALGL 585						
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searched: 12783 seqs, 47026705 residues						
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post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 45 summaries						
Database : SwissProt_41:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.						
SUMMARIES						
	result No.	Score	Query Match	Length	DB ID	Description
1	3103	100.0	609	1	ALBU_HUMAN	P02768 homo sapiens
2	2942	94.8	600	1	ALBU_MACACA	P02822 macaca fasciata
3	2630	84.4	608	1	ALBU_FELINA	P49664 felis sylvestris
4	2562	82.6	608	1	ALBU_CANINA	P49622 canis lupus
5	2745.5	79.8	607	1	ALBU_BOREALIS	P49617 equus caballus
6	2450.5	79.0	607	1	ALBU_BOVINUS	P02769 bos taurus
7	2444.6	78.8	608	1	ALBU_RABBIT	P49665 oryctolagus cuniculus
8	2432.5	78.4	607	1	ALBU_SHEEP	P14339 ovis aries
9	2426	78.2	608	1	ALBU_BEAR	P02770 ursus arctos
10	2411.5	77.7	605	1	ALBU_PIG	P08335 sus scrofa
11	2387	76.9	609	1	ALBU_MERINUS	P03590 meriones
12	2378	76.6	608	1	ALBU_MOUSE	P07724 mus musculus
13	1557.5	50.2	615	1	ALBU_CHICK	P19121 gallus gallus
14	1253.5	40.4	609	1	FETA_PANTHERA	P02772 panthera pardus
15	1249.5	40.3	609	1	FETA_HUMAN	P02771 homo sapiens
16	1242.5	40.0	609	1	FETA_GORILLA	P28050 gorilla gorilla
17	1205	38.8	607	1	ALB2_XENIA	P14878 xenopus laevis
18	1200	38.7	609	1	FETA_HORSE	P49666 equus caballus
19	1164.5	37.5	606	1	ALB1_XENIA	P02859 xenopus laevis
20	1084	34.9	605	1	FETA_MOUSE	P02772 mus musculus
21	1067	34.4	611	1	FETA_RAT	P02773 rattus norvegicus
22	1055	34.0	599	1	AFAM_HUMAN	P43552 homo sapiens
23	944	30.4	611	1	AFAM_MOUSE	P08920 mus musculus
24	928	29.9	608	1	AFAM_RAT	P3653 ratmus rattus
25	747.5	24.1	608	1	ALBL_SALSA	P21448 salmo salar
26	742.5	23.9	608	1	ALB2_SALSA	Q03156 salmo salar
27	699	22.5	382	1	ALBU_RANCA	P21447 ranunculus
28	440.5	14.2	1423	1	ALBU_PETMA	Q91274 petromyzon marinus
29	386	12.4	474	1	VTDB_HUMAN	P02774 homo sapiens
30	381	12.3	476	1	VTDB_RAT	P04746 rattus norvegicus
31	378	12.2	476	1	VTDB_RABBIT	P53899 oryctolagus cuniculus
32	372	12.0	476	1	VTDB_MOUSE	P21514 mus musculus
33	151.5	4.9	1605	1	RRB1_MOUSE	O99151 mus musculus

34	144.5	4.7	8797	1	SNE1_HUMAN	Q8nf91	homo sapien
35	138.5	4.5	1410	1	RRB1_HUMAN	Q9p289	homo sapien
36	133.5	4.3	1391	1	MST2DROHY	Q08696	drosophila
37	132.5	4.3	2230	1	GOG4_HUMAN	Q13439	homo sapien
38	129.5	4.2	1972	1	MTHB_HUMAN	P35749	homo sapien
39	129	4.2	3105	1	CENF_HUMAN	P44244	homo sapien
40	128	4.1	1005	1	RA50_MEJUA	Q58718	methanococc
41	126.5	4.1	1972	1	MTHB_RABIT	P35748	oryctolagus
42	126	4.1	1189	1	SMC2_CHICK	Q09988	galus galli
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44	125	4.0	3038	1	TRIO_HUMAN	Q75962	homo sapien
45	124.5	4.0	1790	1	USO1_YEAST	P25386	saccharomy
ALIGNMENTS							
RESULT 1							
ALBU_HUMAN			STANDARD;	PRT;	609 AA.		
ID			Q95574;	Q13140;			
AC			Q9P157;	Q9P117;	Q9UHS3;	Q9UTU0;	
DT	21-JUL-1986	(Rel. 01, Created)					
DT	01-APR-1990	(Rel. 14, Last sequence update)					
DT	15-SEP-2003	(Rel. 42, Last annotation update)					
DE	Serum albumin precursor.						
GN							
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.						
OX							
NCBI_TAXID=9606;							
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=6195112;		PubMed=3009475;				
RA	Minghetti P.P., Rufner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,						
RA	Beattie W.G., Dugaiczyk A.;						
RT	"Molecular structure of the human albumin gene is revealed by						
RT	nucleotide sequence within q11-22 of chromosome 4.";						
RL	J. Biol. Chem. 261:6747-6757(1986).						
RN	[2]						
RP	SEQUENCE FROM N.A. AND VARIANT LYS-420.						
RX	MEDLINE=20281882;		PubMed=6171778;				
RA	Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,						
RA	Najarian R.C., Seебrig P.H., Wion K.L.,						
RT	"The sequence of human serum albumin cDNA and its expression in E. coli."						
RT	Nucleotide sequence and the encoded amino acids of human serum albumin mRNA."						
RL	Nucleic Acids Res. 9:6103-6114(1981).						
RN	[3]						
RP	SEQUENCE FROM N.A. AND VARIANT GLY-121.						
RX	MEDLINE=22105994;		PubMed=6275391;				
RA	Dugaiczyk A., Law S.W., Dennison O.E.;						
RT	"Nucleotide sequence and the encoded amino acids of human serum albumin mRNA."						
RT	Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982).						
RN	[4]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Fetal liver;						
RA	Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;						
RA	Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,						
RA	Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Liu L.;						
RT	"Functional prediction of human serum albumin";						
RT	deduced by analysis of cDNA clones from human fetal liver."						
RL	Submitted (FBB-1999) to the EMBL/GenBank/DBJ databases.						
RN	[5]						
RP	SEQUENCE FROM N.A. AND VARIANT GLY-121.						
RC	Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,						
RA	Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Liu L.;						
RA	"The cDNA sequences of human serum albumin";						
RT	Submitted (AGB-2002) to the EMBL/GenBank/DBJ databases.						
RL	[6]						
RP	SEQUENCE FROM N.A. AND VARIANT HIROSHIMA-1 LYS-378.						
RA	Huang M.C., Wu H.T.;						
RA	"The cDNA sequences of human serum albumin";						
RT	Submitted (AGB-2002) to the EMBL/GenBank/DBJ databases.						
RL	[7]						
RP	SEQUENCE FROM N.A.						

RC TISSUE="Liver, and Skeletal muscle;
MEDLINE=22388257; PubMed=1247792;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schneich A., Schein J.E., Jones J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [8]

RP SEQUENCE OF 25-609.
RX MEDLINE=1225573;

RA Brown J.R., Shockley P., Behrens P.Q.,
RL (In) Bing D.H. (eds.);
RL The chemistry and physiology of the human plasma proteins, pp.23-40,
RA Melton B., Moravek L., Kostka V.,
RT "Complete amino acid sequence of human serum albumin.",
RL FEBS Lett. 58:134-137(1975).
RN [9]

RP SEQUENCE OF 25-609.
RX MEDLINE=16187907; PubMed=1225573;

RA Urano Y., Watanae K., Sakai M., Tamaoki T.,
RT "The human albumin gene. Characterization of the 5' and 3' flanking
RT regions and the polymorphic gene transcripts.",
RL J. Biol. Chem. 251:3244-3251(1986).
RN [11]

RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=96140099; PubMed=2419329;

RA Manaya J., Parrilla R., Ayuso M.S.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [11]

RP SEQUENCE OF 222-229.
RX MEDLINE=76257808; PubMed=955075;

RA Walker J.E.;
RA RT "Lysine residue 199 of human serum albumin is modified by
RT acetyl-salicylic acid.",
RL FEBS Lett. 66:173-175(1976).
RN [13]

RC TISSUE=Heart;
RA MEDLINE=95203287; PubMed=7895732;

RA Corbett J.M., Wheeler C.H., Baker C.S., Yacob M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.",
RL Electrophoresis 15:1459-1465(1994).
RN [14]

RP DISULFIDE BONDS.
RA Saber M.A., Stockbauer P., Moravek L., Meloun B.;
RT "Disulfide bonds in human serum albumin.",
RL Collect. Czech. Chem. Commun. 42:564-579(1977).
RN [15]

RP BILIRUBIN-BINDING SITE.
RX MEDLINE=78186630; PubMed=656055;

RA Jacobsen C.;
RT "Lysine residue 240 of human serum albumin is involved in high-
affinity binding of bilirubin.",
RL Biochem. J. 171:453-459(1978).

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RN VARIANT CANTERBURY ASN-337;
RP MEDLINE=87157744; PubMed=828358;
RX Brennan S.O., Herbert P.;
RA Herbert (3.13 Asn--Asn). A point mutation in the second
RA domain of serum albumin.";
RT Blochim. Biophys. Acta 912:191-197(1987).
RN [17]

RN VARIANT NAG-2 AND NAG-3;
RP MEDLINE=88068533; PubMed=3479777;
RX Takanashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
RA Satoch C., Neel J.V.;
RA Satoch C., Neel J.V.;
RT "Amino acid substitutions in inherited albumin variants from
RT American and Japanese populations.";
RT Amerindian and Japanese populations.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
RN [18]

RN VARIANT NAG-1, HIR-1, HIR-2 AND TOCHIGI.
RP MEDLINE=8945611; PubMed=2762316;
RX Satoch C., Neel J.V.;
RA Satoch C., Neel J.V.;
RA Arai K., Madison J., Russ K., Ishioka N., Satoh C., Fujita M.,
RA Neel J.V.;
RT "Point substitutions in Japanese alloalbumins.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
RN [19]

RN VARIANT MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
RP MEDLINE=90115905; PubMed=2404284;

RA MEDLINE=90115906; PubMed=2404285;

RA Arai K., Madison J., Shimizu A., Putnam F.W.,
RA Arai K., Madison J., Shimizu A., Putnam F.W.,
RT "Point substitutions in albumin genetic variants from Asia.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
RN [20]

RN DESCRIPTION OF VARIANT REDHILL.
RP MEDLINE=90115832; PubMed=2104930;

RA MEDLINE=90115833; PubMed=2104931;

RA Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
RA Arai K., Madison Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of
RT human serum albumin whose precursor has an aberrant signal peptidase
RT cleavage site";
RL Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
RN [21]

RN VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
RP MEDLINE=90115834; PubMed=2104940;

RA MEDLINE=91062332; PubMed=2247440;

RA Watkins S., Galliano M., Manchietto L., Porta F., Rossi A., Ferri G., Madison J.,
RA Watkins S., Galliano M., Manchietto L., Porta F., Rossi A., Ferri G., Madison J.,
RT "Albumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of
RT human serum albumin whose precursor has an aberrant signal peptidase
RT cleavage site";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
RN [22]

RN VARIANT VENEZIA.
RP MEDLINE=9129670; PubMed=2068071;

RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
RT "A donor splice mutation and a single-base deletion produce two
RT carboxyl-terminal variants of human serum albumin.",
RL Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN [23]

RN VARIANT IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23;

RP KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.

RA Watkins S., Galliano M., Manchietto L., Porta F.W.,
RA Watkins S., Galliano M., Manchietto L., Porta F.W.,
RT "A donor splice mutation and a single-base deletion produce two
RT carboxyl-terminal variants of human serum albumin.",
RA Watkins S., Galliano M., Manchietto L., Porta F.W.,
RA Watkins S., Galliano M., Manchietto L., Porta F.W.,
RT "Genetic variants of serum albumin in Americans and Japanese.",
RL Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
RN [24]

RN VARIANT CASPERBOOK ASN-518;
RP MEDLINE=91316157; PubMed=1859851;

RA Peach R.J., Brennan S.O.;
RT "Structural characterization of a glycoprotein variant of human serum
RT albumin: albumin Casebrook (494 Asp-->Asn).";
RL Biochim. Biophys. Acta 1097:49-54(1991).

RN VARIANT SONDRIO LYS-357 AND PARIS-2 ASN-587.
RP MEDLINE=92190239; PubMed=1347703;

RA Minchietto L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
RA Rock D., Porta F.,
RT "Two alloalbumins with identical electrophoretic mobility are produced

Query Match 100.0%; Score 3103; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 1.7e-194;
 Nmatches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHREPKDGEENFKALVIAQYLOQCPEDHVKLVNTEFAKTCVADSEAE 60
 Db 25 DAHKSEVAHREPKDGEENFKALVIAQYLOQCPEDHVKLVNTEFAKTCVADSEAE 84

Qy 61 NCDSLTHLFGDKCTVATLRLTYGEMADCAKEOPERNECFCLOHDDNPNLPLVREPV 120
 Db 85 NCDSLTHLFGDKCTVATLRLTYGEMADCAKEOPERNECFCLOHDDNPNLPLVREPV 144

Qy 121 DYMCTAFAHDEETFLKLYTETARRHPPYTAPELLEFFKRYKAAFFTECCOAADKAACLPL 180
 Db 145 DYMCTAFAHDEETFLKLYTETARRHPPYTAPELLEFFKRYKAAFFTECCOAADKAACLPL 204

Qy 181 KLDDELDEGRASSAKQRLKCALQKGERAFKAWAVALSRQPKAAFEAVSKLYTDLTK 240
 Db 205 KLDDELDEGRASSAKQRLKCALQKGERAFKAWAVALSRQPKAAFEAVSKLYTDLTK 264

Qy 241 VTEECGHGDLLECADDRADLAKYTCNODSISSSKKECECPLESHCTAEVENDPMA 300
 Db 265 VTEECGHGDLLECADDRADLAKYTCNODSISSSKKECECPLESHCTAEVENDPMA 324

Qy 301 DIPSLLAADFVEISKVCKRNAYAKDFIGMFLYEFARRHPPDSVLLRLAKKTTETLKC 360
 Db 325 DIPSLLAADFVEISKVCKRNAYAKDFIGMFLYEFARRHPPDSVLLRLAKKTTETLKC 384

Qy 361 CAAADPHCAYKVDPEKFPLVPEQPNLLIKCONELFOLGEYKFTQNALVRYTKVPOYST 420
 Db 385 CAAADPHCAYKVDPEKFPLVPEQPNLLIKCONELFOLGEYKFTQNALVRYTKVPOYST 444

Qy 421 PTVVEYSRNIGKVGSKCCKHPEAKRMPCAEDYLSVSLAQCVLHETPTPSDRTKCTBS 480
 Db 445 PTVVEYSRNIGKVGSKCCKHPEAKRMPCAEDYLSVSLAQCVLHETPTPSDRTKCTBS 504

Qy 481 LYNNRPOPSALEDETYVKPKEAETTFRADICLSEKERQIKKQTALEYLVKHPKAT 540
 Db 505 LYNNRPOPSALEDETYVKPKEAETTFRADICLSEKERQIKKQTALEYLVKHPKAT 564

Qy 541 KEGOLKAVMDDEAFAVEKCKADDKETQFAEKGKKVIAASQAAIGL 585
 Db 565 KEGOLKAVMDDEAFAVEKCKADDKETQFAEKGKKVIAASQAAIGL 609

RESULT 2
 ALBU_MACMU STANDARD; PRT; 600 AA.
 AC Q28522;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Serum albumin precursor (Fragment).
 GN Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Cercopithecidae; Macacidae.
 RN NCBI_TaxID:9544;
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93211971; PubMed=8460152;
 RA Watkins S.A., Sakamoto Y., Nadiron J.M., Davis E.M., Smith D.G.,
 DWulet J., Putnam F.W.;
 RT "cDNA and protein sequence of polymorphic macaque albumins that differ
 in bilirubin binding";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2409-2413 (1993).
 CC - FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+) fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidal osmotic pressure of blood.
 CC - SUBCELLULAR LOCATION: Secreted.

- TISSUE SPECIFICITY: Plasma.
 - SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC - SIMILARITY: Contains 3 albumin domains.

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DR EMBL; M50463; AAA36906; 1;
 DR PIR; A41391; A41391.
 DR HSSP; P02768; IEBB.
 DR InterPro; IPR00264; Serum albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; P00806; SEROMALBUMIN.
 DR ProDom; PD002486; Serum albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 RW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 DR Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL <1 1 BY SIMILARITY.
 FT PROPEP 1 10 BY SIMILARITY.
 FT CHAIN 1 16 BY SIMILARITY.
 FT DOMAIN 1 197 ALBUMIN 1.
 FT DOMAIN 2 204 389 ALBUMIN 2.
 FT DOMAIN 3 396 587 ALBUMIN 3.
 FT METAL 1 19 COPPER (BY SIMILARITY).
 FT BINDING 256 256 BILIRUBIN (POTENTIAL).
 FT DISULFID 69 78 BY SIMILARITY.
 FT DISULFID 91 107 BY SIMILARITY.
 FT DISULFID 106 117 BY SIMILARITY.
 FT DISULFID 140 185 BY SIMILARITY.
 FT DISULFID 184 193 BY SIMILARITY.
 FT DISULFID 216 262 BY SIMILARITY.
 FT DISULFID 261 269 BY SIMILARITY.
 FT DISULFID 281 295 BY SIMILARITY.
 FT DISULFID 294 305 BY SIMILARITY.
 FT DISULFID 332 377 BY SIMILARITY.
 FT DISULFID 376 385 BY SIMILARITY.
 FT DISULFID 408 454 BY SIMILARITY.
 FT DISULFID 453 464 BY SIMILARITY.
 FT DISULFID 477 493 BY SIMILARITY.
 FT DISULFID 492 503 BY SIMILARITY.
 FT DISULFID 530 575 BY SIMILARITY.
 FT DISULFID 574 583 BY SIMILARITY.
 SQ SEQUENCE 600 AA; 67880 MW; E45C87LA670E740B CRC64;

Query Match 94.0%; Score 2342; DB 1; Length 600;
 Best Local Similarity 93.5%; Pred. No. 4.8e-184;
 Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHREPKDGLBENKALVYLAQYLOQCPPEHDHYKLYNEYTHFAKTCVADSEAE 60
 Db 17 DTHKSEVAHREPKDGLBENKALVYLAQYLOQCPPEHDHYKLYNEYTHFAKTCVADSEAE 76

Qy 61 NCDSLTHLFGDKLCTVATLRETYGEMADCAKQPERNECFCQHQDNPNLPLVRYPEV 120
 Db 77 NCDSLTHLFGDKLCTVATLRETYGEMADCAKQPERNECFCQHQDNPNLPLVRYPEV 136

Qy 121 DVMTCAFHDNEETFLKLYTETARRHPPYTAPELLEFFKRYKAAFFTECCOAADKAACLPL 180
 Db 137 DVMTCAFHDNEETFLKLYTETARRHPPYTAPELLEFFKRYKAAFFTECCOAADKAACLPL 196

Qy 181 KLDDELDEGRASSAKQRLKCALQKGERAFKAWAVALSRQPKAAFEAVSKLYTDLTK 240
 Db 197 KLDDELDEGRASSAKQRLKCALQKGERAFKAWAVALSRQPKAAFEAVSKLYTDLTK 256

Qy 241 VTEECGHGDLLECADRADLAKYTCNODSISSSKKECECPLESHCTAEVENDPMA 300
 Db 257 VTEECGHGDLLECADRADLAKYTCNODSISSSKKECECPLESHCTAEVENDPMA 316

QY	541	KEQIKAVAMDDPRAFTEKCCADDKETGFAERGKLVAAASQAAI	583	
Db	565	DEQIKTVAGDEGAFETEKCCAENKEGCFSEEGPKLVAAASQAAI	607	
	RESULT 5			
	ALBU_HORSE	STANDARD;	PRT;	607 AA.
	ID			
	AC	P35747;		
	DT	01-JUN-1994 (Rel. 29, Created)		
	DT	01-JUN-1994 (Rel. 29, Last sequence update)		
	DT	28-FEB-2003 (Rel. 41, Last annotation update)		
	DE	serum albumin precursor.		
	GN	ALB.		
	OS	Equus caballus (Horse).		
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
	OX	NCBL_TaxID=996;		
	RN			
	RP	SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).		
	RC	TISSUE=Liver; PDBID=1J49; PubMED=8344282;		
	RX	Medline:93315495; PubMed=8344282;		
	RA	Ho J.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;		
	RT	"X-ray and primary structure of horse serum albumin (Equus caballus)		
	RT	"		
	RL	EUR. J. Biochem. 215:205-212(1993).		
	CC	-1- FUNCTION: Serum albumin, the main protein of plasma, has a good		
	CC	binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,		
	CC	hormones, bilirubin and drugs. Its main function is the regulation		
	CC	of the colloidal osmotic pressure of blood.		
	CC	-1- SUBCELLULAR LOCATION: Plasma.		
	CC	-1- TISSUE SPECIFICITY: BELONGS TO THE ALB/APP/VDB FAMILY.		
	CC	-1- SIMILARITY: Contains 3 albumin domains.		
	CC	-----		
	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
	CC	the European Bioinformatics Institute. There are no restrictions on its		
	CC	use by non profit institutions and the EMBL outstation -		
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	CC	entities requires license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
	CC	-----		
	DR	EMBL: X74045; CAA52194.1; -.		
	DR	HSSP: S34053; ABHOS.		
	DR	InterPro: IPR000264; Serum_albumin.		
	DR	PRINTS: PF00273; transport_prot; 3.		
	DR	PRINTS: PRO0002; SERMALBUMIN.		
	DR	ProDom: PD000486; Serum_albumin; 1.		
	DR	SMART; SM0103; ALBUMIN; 3.		
	DR	PROSITE; PS00212; ALBUMIN; 3.		
	KW	Metal-binding; Lipid-binding; Repeat; Signal; Copper.		
	FT	SIGNAL 1 18 BY SIMILARITY.		
	FT	PROPEP 19 24 BY SIMILARITY.		
	FT	CHAIN 25 607 SERUM ALBUMIN.		
	FT	DOMAIN 25 204 ALBUMIN 1.		
	FT	DOMAIN 211 396 ALBUMIN 2.		
	FT	DOMAIN 403 594 ALBUMIN 3.		
	FT	METAL 27 27 COPPER (BY SIMILARITY).		
	FT	DISULFID 77 86		
	FT	DISULFID 99 115		
	FT	DISULFID 114 125		
	FT	DISULFID 147 192		
	FT	DISULFID 191 200		
	FT	DISULFID 223 223		
	FT	DISULFID 268 276		
	FT	DISULFID 288 302		
	FT	DISULFID 301 312		
	FT	DISULFID 339 384		
	FT	DISULFID 383 392		
	FT	DISULFID 415 415		

FT	DISULFID	460	471	
FT	DISULFID	484	500	
FT	DISULFID	499	510	
FT	DISULFID	537	582	
FT	DISULFID	581	590	
SQ	SEQUENCE	607 AA;	68598 MW;	256F6E830A1B90C5 CRC64;
	Query Match	79.8%	Score 2475.5;	DB 1; Length 607;
	Best Local Similarity	76.3%	Pred. No. 9.8e-154;	
	Matches	445;	Conservative	69; Mismatches 68; Indels 1; Gaps 1;
QY	1	DAHKSEVAHREFDGLBENKVALYIAPQYLQQCPPEHDYKLYNEVTEFACTCYADESAE 60		
DB	25	DTHRSEAHRENDLGEKHKGLVIVASQYLQQCPPEHDYKLYNEVTEFAKCAADESAE 84		
GN	61	NCDKSLHFLFGDKLCTVATLRETGYEMDCCAKQEPERNECFLQHDDNPNLPRYRPEV 120		
OS	85	NCDKSLHFLFGDKLCTVATRATYGEFLDCCKQEPERNECFLTHDKPFLK -KPF 143		
OC	121	DVMCTAHDNEETFLKLYIETARRHPTYAPELLFAKRYKAFTECQADKAACLLP 180		
OC	144	DACQAARFBDPKFLGKLYIETARRHPTYAPELLFAKRYKAFTECQADKAACLLP 203		
RT	181	KLDELDRDGKASSAKORLKCAASLQKFGRAFAWARYLSQRFQPKAEPAEVSKYDILK 240		
RT	204	KLDALKRILISSAKERLKCSSONFGRAYKAWARYLSQPKFQDAEPAEVSKYDILK 263		
RL	241	VRTECCCHGDLCAADRDLAKYICENDTSSKKECCKPKLEKSHCIAEVENDEMA 300		
CC	264	VHKRCCHGDLCAADRDLAKYICENDTSSKKECCKPKLEKSHCIAEVKEDDLSS 323		
CC	301	DLPSSIAQEVESKDVKNYAFAKYVFLGMLFLEYARRHPTYSVLLRKAFTYETLEKC 360		
CC	324	DLPALADFAEDEKICHHYDKAQYFLGTFLEYSPRHPDYSVLLRKAFTYETLEKC 383		
CC	351	CAAADPHECYAKVFEDEKPKLVEPONLQKNCBFLPQGEYKPNONLLVRTTKKPVQST 420		
CC	384	CAEADPACYRIVDQTPLYEVEKSLKKNCDLFEVGEGYDFNALLYRTTKKAPQST 443		
CC	421	PTLVESYRNLGKVGSCKQPKAEPQADYLSSVNLQCVLIEKETVSDVXTCCTES 480		
CC	444	PTLVIGRLGKVGSCKQPKAEPESRLPSENHIALNLNCVLEHKTPVSEKTRCCDTS 503		
CC	481	LYNRRPCFSALEYDTPYKEFNAETEFDADICLSEKQTKQTALEVLYKHPKAT 540		
CC	504	LAERPCFSALEDEGGVPRKETAFTHADICLSEKQTKQTALEVLYKHPKAT 563		
CC	541	KEQIKAVAMDDEAFAVKEKCADKETCPAEGKLYAAASQAAI 583		
CC	564	KEQIKTVGNSFAVAKCCGREKDAECPKLYVASSQIAI 606		

RESULT 6				
ALBU_BOVIN				
ID				
AC	P02769; 002787;	STANDARD;	PRT;	607 AA.
AC				
DT	21-JUN-1986 (Rel. 01, Created)			
DT	01-FEB-1986 (Rel. 33, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Serum albumin precursor (Allergen Bos d 6).			
GN	ALB.			
OS	Bos_taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Bos.			
OC	NCBI_TaxID=9913;			
OX				
RN	SEQUENCE FROM N.A.			
RN	[1]			
RN	Hollowchuk E.W., Stoiltenborg J.K., Reed R.G., Peters T. Jr.,			
RN	[2]			
RP	Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A., AND VARIANT THR-214.			
RC	TISSUE=Liver;			

RA Barry T., Power S., Gannon F.; Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-Liver;

RA Hiltiger C., Gridioni F., de Beaufort C., Michel G., Hentges F.; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A., AND VARIANT THR-214.

RN [5]

RA Wu H.T., Huang M.C.; RT The complete cDNA sequence of bovine serum albumin.;

RA "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of prealbumin";

RT PROTEIN; PRO0802; SERUMALBUMIN.

RL EUR. J. Biochem. 98:477-485(1979).

RN [6]

RA SEQUENCE OF 25-124 AND 429-607, AND VARIANT THR-214.

RA Brown J.R.; RT "Structure of bovine serum albumin.";

RL Proc. 34:591-591(1975).

RN [7]

RP REVISIONS TO 190-195.

RA Brown J.R.; RT Submitted (APR-1975) to the PIR data bank.

RN [8]

RP SEQUENCE OF 402-433.

RX MEDLINE-82023364; PubMed=7283978;

RA Reed R.G., Putnam F.W., Peters T. Jr.;

RA "Sequence of residues 400-403 of bovine serum albumin.;"

RL Biochem. J. 191:867-868(1980).

RN [9]

RP SEQUENCE OF 19-28.

RX MEDLINE=71134075; PubMed=843354;

RA Patterson J. E., Geller D.M.;

RT "Bovine microsomal albumin: amino terminal sequence of bovine proalbumin.";

RA Biochem. Biophys. Res. Commun. 74:1220-1226(1977).

RN [10]

RP SEQUENCE, AND REVISIONS TO 118-119 AND 180.

RX MEDLINE-91033649; PubMed=2260975;

RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;

RT "Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";

RA Biochem. Biophys. Res. Commun. 173:639-646(1990).

RN [11]

RP SEQUENCE OF 25-41.

RX MEDLINE-88287456; PubMed=3389500;

RA Hsieh J.C., Lin F.P., Tam M.F.;

RT "Electroblotting onto glass fiber filter from an analytical isoelectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";

RT Anal. Biochem. 170:1-8(1988).

RN [12]

RP SEQUENCE OF 437-451.

RA Vilbois F.; RT Submitted (AUG-1998) to the SWISS-PROT data bank.

RN [13]

RP DISULFIDE BONDS.

RA Brown J.R.;

RT "Structure of serum albumin: disulfide bridges.";

RL Fed. Proc. 33:1389-1389(1974).

CC - FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca^{2+} , Na^{+} , K^{+} , fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CC - SUBCELLULAR LOCATION: Secreted.

CC - TISSUE SPECIFICITY: Plasma.

CC - SIMILARITY: BELONGS TO THE ALB/APP/YDB FAMILY.

CC - SIMILARITY: Contains 3 albumin domains.

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CC SEQUENCE FROM N.A., AND VARIANT THR-214.

CC Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

RP SEQUENCE OF 1-32.

RX MEDLINE-80024278; PubMed=488105;

RA McGillivray R.T.A., Chung D.W., Davie E.W.;

RA "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of prealbumin";

RT PROTEIN; PRO02438; SERUMALBUMIN.

RL SMART: SM00103; ALBUMIN: 3.

RN [14]

RA PROSITE; PS00212; ALBUMIN: 3.

RA PROSITE; PS00212; ALBUMIN: 3.

RN [15]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [16]

RA PROSITE; PS00212; ALBUMIN: 3.

RA PROSITE; PS00212; ALBUMIN: 3.

RN [17]

RP SEQUENCE OF 25-124 AND 429-607, AND VARIANT THR-214.

RA Brown J.R.;

RT "Structure of bovine serum albumin.";

RL Proc. 34:591-591(1975).

RN [18]

RP REVISIONS TO 190-195.

RA Brown J.R.; RT Submitted (APR-1975) to the PIR data bank.

RN [19]

RP SEQUENCE OF 402-433.

RX MEDLINE-82023364; PubMed=7283978;

RA Reed R.G., Putnam F.W., Peters T. Jr.;

RA "Sequence of residues 400-403 of bovine serum albumin.;"

RL Biochem. J. 191:867-868(1980).

RN [20]

RP SEQUENCE OF 19-28.

RX MEDLINE=71134075; PubMed=843354;

RA Patterson J. E., Geller D.M.;

RT "Bovine microsomal albumin: amino terminal sequence of bovine proalbumin.";

RA Biochem. Biophys. Res. Commun. 74:1220-1226(1977).

RN [21]

RP SEQUENCE, AND REVISIONS TO 118-119 AND 180.

RX MEDLINE-91033649; PubMed=2260975;

RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;

RT "Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";

RA Biochem. Biophys. Res. Commun. 173:639-646(1990).

RN [22]

RP SEQUENCE OF 25-41.

RX MEDLINE-88287456; PubMed=3389500;

RA Hsieh J.C., Lin F.P., Tam M.F.;

RT "Electroblotting onto glass fiber filter from an analytical isoelectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";

RT Anal. Biochem. 170:1-8(1988).

RN [23]

RP SEQUENCE OF 437-451.

RA Vilbois F.;

RA Submitted (AUG-1998) to the SWISS-PROT data bank.

RN [24]

RP DISULFIDE BONDS.

RA Brown J.R.;

RT "Structure of serum albumin: disulfide bridges.";

RL Fed. Proc. 33:1389-1389(1974).

CC - FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca^{2+} , Na^{+} , K^{+} , fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CC - SUBCELLULAR LOCATION: Secreted.

CC - TISSUE SPECIFICITY: Plasma.

CC - SIMILARITY: BELONGS TO THE ALB/APP/YDB FAMILY.

CC - SIMILARITY: Contains 3 albumin domains.

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CC SEQUENCE FROM N.A., AND VARIANT THR-214.

CC Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [25]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [26]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [27]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [28]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [29]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [30]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [31]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [32]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [33]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [34]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [35]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [36]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [37]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [38]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [39]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [40]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [41]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [42]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [43]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [44]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [45]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [46]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [47]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [48]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [49]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [50]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [51]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [52]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [53]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [54]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [55]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [56]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [57]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [58]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [59]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [60]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [61]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [62]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [63]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [64]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [65]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [66]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [67]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [68]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [69]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [70]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [71]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [72]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [73]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [74]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [75]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [76]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [77]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [78]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [79]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [80]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [81]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [82]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [83]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [84]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [85]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [86]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [87]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [88]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [89]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [90]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [91]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [92]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [93]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [94]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [95]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [96]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [97]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [98]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [99]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [100]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [101]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [102]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [103]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot; 3.

RA PRINTS; PRO0802; SERUMALBUMIN.

RL PRODOM; PD02438; Serum_albumin; 1.

RN [104]

RP SEQUENCE OF 1-32.

RX IPR00264; Serum albumin.

RA Pfam: PF00273; transport_prot;

				SERUM ALBUMIN.
FT	CHAIN	25	608	
FT	DOMAIN	25	205	ALBUMIN 1.
FT	DOMAIN	212	397	ALBUMIN 2.
FT	DOMAIN	404	595	ALBUMIN 3.
FT	METAL	27	27	COPPER.
FT	DISULFID	77	86	BY SIMILARITY.
FT	DISULFID	99	115	BY SIMILARITY.
FT	DISULFID	114	125	BY SIMILARITY.
FT	DISULFID	148	193	BY SIMILARITY.
FT	DISULFID	192	201	BY SIMILARITY.
FT	DISULFID	224	270	BY SIMILARITY.
FT	DISULFID	269	277	BY SIMILARITY.
FT	DISULFID	289	303	BY SIMILARITY.
FT	DISULFID	302	313	BY SIMILARITY.
FT	DISULFID	340	385	BY SIMILARITY.
FT	DISULFID	384	393	BY SIMILARITY.
FT	DISULFID	416	462	BY SIMILARITY.
FT	DISULFID	461	472	BY SIMILARITY.
FT	DISULFID	485	501	BY SIMILARITY.
FT	DISULFID	500	511	BY SIMILARITY.
FT	DISULFID	538	583	BY SIMILARITY.
FT	DISULFID	582	591	BY SIMILARITY.
SQ	SEQUENCE	608 AA;	68914 MW;	CF592647AAF.
Query Match		78.8%	Score: 2446.1	D
Best Local Similarity		74.1%	Pred. No. 8.1e	D
Matches	433; Conservative	77;	Mismatches	
QY	1	DAHKSEYAHFRKFIDIGEENFKALVYTAFAQYOLQOC		
Db	25	EHAKSLAHHFNPNDGEHBFIGVLITFSQIQLRC		
QY	61	NCDKSLHTEFLGDKLCTATVLTRETYGEMADCCAKO		
Db	85	NCDKSHDITGDKICAFKPLRITYGDVADCEKCK		
QY	121	DYCATKAFHDNEETFLKXLYEARHPPYTAPEL		
Db	145	DYLCRAFHDEKAFGHFLYLYEARHPPYTAPEL		
QY	181	KIDELDEKGKASSAKQRLKCAQSLEQGERAFKAWA		
Db	205	KIDALRGKSLISQAERLQRCISQIYQFGDRYKAW		
QY	241	VHTECCHGDLLECADDRADLAKYICENODSISSK		
Db	265	VKECCCHGDLLECADDRADLAKYMEHQETISSEH		
QY	301	DPLSLAADEFVSKVCKNAYAFAKDYLGLGMFLYY		
Db	325	GPAPAEFFEDKQVCKNYPEAKDYLGLGFLYEV		
QY	361	CAADPPECYAKVDEDEKFPLVVEPQNLIKONCEL		
Db	385	CATDDPHACTAKVDEDFPLVDEPKNLVQNCEL		
QY	421	PTIVELVSNLIGKVSCKKHPKAQMPACDYLUS		
Db	445	PTIVELSRSLGKVSSCKKHPKAERLPCVYDYLUS		
QY	481	LYNRRPCSEALEVDETYPKFKEENAEFTFHADIC		
Db	505	LSNRRPCFSALGPDETYPKFKEENAEFTFHADIC		
QY	541	KFQKAWMDDFAAVFKCKKADDKETCFABEGKKG		
Db	565	NFQKLYVGGFTTALDKCCSAEDKRCAPVEGPR		

RT Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage of rat serum albumin.;
 RT J. Biochem. 83:35-48(1978).
 RL [4]
 RN SEQUENCE OF 223-288 AND 572-608.
 RP MEDLINE=16260153; PubMed=956149;
 RX RA Isenura S.; Ichihara T.;
 RA Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.;
 RL J. Biochem. 79:1183-1195(1976).
 RN [5]
 RP SEQUENCE OF 166-174.
 RC TISSUE=Plasma;
 RX MEDLINE=87194805; PubMed=2437111;
 RA Carraway R.E.; Mitra S.P.; Cochrane D.E.;
 RT "Structure of a biologically active neurotensin-related peptide obtained from a peptide secreted albumin(s).";
 RL J. Biol. Chem. 262:5968-5973(1987).
 RN [6]
 RP COPPER-BINDING.
 RX MEDLINE=9001617; PubMed=80265;
 RA Aoyagi Y.; Ikenaka T.; Ichihara F.;
 RT Copper (II)-binding ability of human alpha-fetoprotein.";
 RL Cancer Res. 38:3483-3485(1978).
 CC -I- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+) fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
 CC -I- FUNCTION: NRP regulates fat digestion, lipid absorption, and blood flow (potential).
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: Plasma.
 CC -I- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -I- SIMILARITY: Contains 3 albumin domains.

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DR EMBL; V01222; CAA4532.1; -.
 DR PTR; A93872; ABRS.
 DR InterPro; IPR000264; Serum_albumin_.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRODOM; PRO0002; SERM0ALBUMIN.
 DR SMART; SM00103; ALBUMIN_3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 608 SERUM ALBUMIN.
 FT PEPTIDE 166 174 NEUROTENSIN-RELATED PEPTIDE.
 FT DOMAIN 25 205 ALBUMIN 1.
 FT DOMAIN 212 397 ALBUMIN 2.
 FT DOMAIN 404 595 ALBUMIN 3.
 FT METAL 27 COPPER.
 FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 269 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 462 BY SIMILARITY.

FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.
 FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 FT VARIANT 262 V->L.
 FT CONFLICT 174 174 Y->L (IN REF. 5).
 SQ SEQUENCE 608 AA; 68718 MW; 5BB497A282411AB7 CRC64;
 Query Match 78.2%; Score 2426; DB 1; Length 608;
 Best Local Similarity 73.4%; Pred. No. 1. 6e-150;
 Matches 428; Conservative 82; Mismatches 73; Indels 0; Gaps 0;
 1 DAHSEWAHRFDLGENEFAVLYLAAQYLQQCPFEDHYKLYNEVTEFAKTCYADESAE 60
 25 EAHSELAHRFDLQHFGFLVIAFQYQKCPTEHKLQYEVTDATKTCVADEN 84
 61 NCDKSLHFLFGDKLCPVATLRETQYGMADCCAKQPERNECFLQHDKDNPNLPLRVPY 120
 85 NCDKSIAPLFGDKLCAPLKLRDNYGELADCAKQPERNECFLQHDKDNPNLPLRVPY 144
 121 DVNGTAFIDNEETELKKLYLETAIRHPPFYYAPLEFFAKKYYKAFTRCQADKAICLIP 180
 145 EAMCTSGQENPFLQHFLYLEVARHPPFYYAPLELLTAYEYNEYLTQCCTEDKACLIP 204
 181 KLDERDEKASSAKORLKASLQKGGRAFKAWAVARLSQRPKFAAEYSKLVDLKK 240
 205 KLDAVKETALVAVRQRMKSSMQRFGRAFKAWAVARMSQRFNAEFAETLKADYVK 264
 241 VHTECCHGDLLECADDRADIAKYATCENDSISSSKUCCEKPLKSHCIAEVENDEMA 300
 265 INKECCCHGDLLECADDRAEALKYMCENCATISKQACCDKPYLQKSQCLAEETEDNPA 324
 301 DLPSIAADEFVKEVKNYEAKIVFLLTFLYSERPDPSYVLLRKYAYTLELC 360
 325 DLPSIAADEFVKEVKNYEAKIVFLLTFLYSERPDPSYVLLRKYAYTLELC 384
 361 CAAADPHPECAYVEDKFPLVPEQPNLQKONCEFLPQLGKPFQKONALYRTKYKPVQSY 420
 385 CAEGDPDPAQYGPVLAEPQLYEEPNLQKTCNELYKLGEGYGFONAVLYRTQKAQVSP 444
 421 PTLVEVSRNLGVKGSKCCKHPEAKRMPAEDYLSSVILQNLQVLEKTPVSDRVTKCCTES 480
 445 PTLYEARNLGVGTRCTLPEARLQPLCVDYLSSAIIQLVHLHEKTPVSEKVTKCGS 504
 481 LVNRCPFSEALEDETYVPEKFNAETHTFADICHTSERKQKQTALEVLKHKPKAT 540
 505 EVERPFCASLTYDETVPKFKAETHTFHDICHTDPDKQIKKQTALEVLKHKPKAT 564
 541 KEQIKAVMDPDAFAFVKCKADKETCPAEGSKKLYAASQAL 583
 565 EDQIKTVMGDFAFVDRCCAADRNCPATEGPNLVARSKAL 607
 RESULT 10
 ALBU_PIG STANDARD; PRT; 605 AA.
 ID ALBU_PIG
 AC P08833; Q29016;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor (Fragment).
 GN ALB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCB-ITaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MDDLINE=87016582; PubMed=317440;
 RA Baldwin G.S.; Weinstock J.;
 RT "Nucleotide sequence of porcine liver albumin.";

QY	181	KLDPLRDEGKASAKORLKCASTQKGERAKTAWAYARISQRFKPAEFAYSKVLYTDLIK	240
QY	182	KIEHLRKVLTSAKORLKCASTQKGERAKTAWAYARISQRFKPAEFAYSKVLYTDLIK	261
Db	202	KIEHLRKVLTSAKORLKCASTQKGERAKTAWAYARISQRFKPAEFAYSKVLYTDLIK	261
QY	241	VTEETCCEDLICADDRADAKLAKTICENODISSKRECCCKPLLEKSHCIAEKDELTA	300
Db	262	VHKCCECHDLICADDRADAKLAKTICENODISSKRECCCKPLLEKSHCIAEKDELTA	321
QY	301	DLPSSLAADFEVEKSYDKVCKYNTAEAKDVLGMFLYEYARRHDPDSYVLLRLAKTYETTLER	360
Db	322	DNLPLERDVEKSYDKVCKYNTAEAKDVLGMFLYEYARRHDPDSYVLLRLAKTYETTLER	381
QY	361	CAADAPHECAYKVEDDFEKPLVEEPOUNLICONCEPEOLGEYKFGONALIVRTKPKVQST	420
Db	382	CAKEDPACAYATFQPLVDEEKNLKLKONCEPEFKLGHGYFGONALIVRTKPKVQST	441
QY	421	PTIVEVEURNLKGKVSGKCKPAEPRMPAEDYLSTVNLQCVLIEKPTVSDRVTKCCTES	480
Db	442	PTLVEVAKLGLGVSRCCKPAEERLSCAEDYLSTVNLQCVLIEKPTVSEKVTKCCTES	501
QY	481	LYNRRPCFSALLEDETYVPKBEFNAETFTTHDICTUSEKEROIKQTALVELYKHKPKAT	540
Db	502	LYNRRPCFSALDPDEYVYKPKFVEGTTFIFHAUDCLTPEDERQIKQTALVELYKHKPKAT	561
QY	541	REKQYAKVADDFAAVFERCCADDECTCPAEEGAKLV	576
Db	562	EQRLTVLGNFAFVQKCCAPDHAECAVGEKFV	597
RESULT 11			
ALBUM_MERUN			
ID	ALBUM_MERUN	STANDARD:	PRT;
AC	035090;		609 AA.
DT	15-JUL-1998	(Rel. 36, Created)	
DT	15-JUL-1998	(Rel. 36, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Serum albumin precursor.		
GN			
OS	Meriones unguiculatus (Mongolian jird)	(Mongolian gerbill).	
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Gerbillinae;		
OC	Meriones.		
OX	NCBI_TaxID:10047;		
RN	1	SEQUENCE FROM N.A.	
RP			
RC			
SPAIN=MGS	IDR; TISSUE=Liver;		
RC	SPAIN=MGS		
RX			
RA	Medline=9455485;		
RA	Pubmed=9455485;		
RA	98116663;		
RA	Seto-Oshima H.; Sinohara H.;		
RA	Yoshimura K.		
RT	Sequencing of cDNA encoding serum albumin and its extrahepatic		
RT	synthesis in the Mongolian gerbil, <i>Meriones unguiculatus</i> ,";		
RL	Res. 4:351-354 (1997).		
CC	-1- FUNCTION: Serum albumin, the main protein of plasma, has a good		
CC	binding capacity for water, Ca^{2+} , Na^+ , K^+ , fatty acids,		
CC	hormones, bilirubin and drugs. Its main function is the regulation		
CC	of the colloidal osmotic pressure of blood.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- TISSUE SPECIFICITY: Plasma		
CC	-1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.		
CC	-1- SIMILARITY: Contains 3 albumin domains.		
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce		
CC	or send an email to license@isb-sib.ch).		
DR	EMBL; AB001197; BAA21765.1; -.		
DR	PIR; JG5838; JG5838.		
DR	HSSP; P02768; 1E7B.		
DR	InterPro; IPR00264; Serum_albumin.		
DR	Pfam; PF00273; transport_prot; 3;		
DR	Pfam; PF00273; transport_prot; 3;		

DR	PRINTS; PRO0802; SERUMALBUMIN.	Db	567 EQLKXVMDFAFPKCKQEDKEACFSTEGPKVVAESQKAL 608
DR	PRODOM; PD007485; Serum albumin; 1.		
DR	SMART; SMART03; ALBUMIN; 3.		
DR	PROSITE; PS0212; ALBUMIN; 3.		
KW	Metal-binding; Lipid-binding; Repeat; Signal; Copper.	RESULT 1.2	
FT	SIGNAL 1 18	ALBU_MOUSE	ALBU_MOUSE
FT	PROTEIN 18	ID	ALBU_MOUSE
FT	BY SIMILARITY.	AC	001802;
FT	BY SIMILARITY.	DT	01-APR-1988 (Rel. 07, Created)
FT	SERUM ALBUMIN.	DT	15-JUL-1999 (Rel. 38, Last sequence update)
FT	ALBUMIN 1.	DT	28-FEB-2003 (Rel. 41, Last annotation update)
FT	ALBUMIN 2.	DE	Serum albumin precursor.
FT	ALBUMIN 3.	GN	ALB OR ALB1 OR ALB-1.
FT	COPPER.	OS	Mus musculus (Mouse)
FT	BY SIMILARITY.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
FT	BY SIMILARITY.	OX	
FT	BY SIMILARITY.	NCBI_TAXID	10090;
FT	BY SIMILARITY.	[1]	
FT	BY SIMILARITY.	RN	
FT	BY SIMILARITY.	RP	SEQUENCE FROM N.A.
FT	BY SIMILARITY.	RC	TISSUE=Liver;
FT	BY SIMILARITY.	RA	van Reeth T., Gabant P., Dreze P., Sapiro J., Szpirer C.;
FT	BY SIMILARITY.	RL	Submitted (SPE-1998) to the EMBL/GenBank/DBJ databases.
FT	BY SIMILARITY.	RN	[2]
FT	BY SIMILARITY.	RP	SEQUENCE FROM N.A.
FT	BY SIMILARITY.	RC	STRAIN=C57BL/6J; TISSUE=tongue;
FT	BY SIMILARITY.	RX	MEDLINE=2108560; PubMed=11217851;
FT	BY SIMILARITY.	RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Kawai J., Shinagawa A., Gojobori T., Boni H., Kasukawa T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kihl P., Lewis S., Matsuo T., Nakaido I., Peso G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blawie J., Boffelli D., Boujunga N., Carninci P., de Bonaldo M.F., Blawie M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzuki H., Satoh K., Schoenbach C., Suya T., Shiba Y., Storch K.-F., Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohutsuki S., Hayashizaki Y.;
FT	BY SIMILARITY.	RA	"Functional annotation of a full-length mouse cDNA collection.";
FT	BY SIMILARITY.	RL	Nature 409:685-690 (2001).
FT	BY SIMILARITY.	RN	[3]
FT	BY SIMILARITY.	RP	SEQUENCE OF 99-516 FROM N.A.
FT	BY SIMILARITY.	RX	MEDLINE=89216123; PubMed=2452956;
FT	BY SIMILARITY.	RA	Minghetti P.-P., Law S.W., Dugiczyk A.;
Db	27 AHKBEIAHRYKDLGKLYFKGSLVLYTFSQYLQKCSYEHVKLYREVTFASNCAKEDSAEN 61	DB	"The rate of molecular evolution of alpha-fetoprotein approaches that of pseudogenes";
QY	27 CDKSLHATGDKLTYATDTEYCAQEPNCFQLEPQYFPEYD 121	RA	RT
QY	62 CDKSLHATGDKLTYATDTEYCAQEPNCFQLEPQYFPEYD 121	RA	RT
DB	87 CDKSLHATGDKLUSLPNFCGKTAEMADCCAKQEPNCFQLEPQYFPEYD 146	RA	RT
QY	122 VMCTAHDNEETFLKXLYTARREHPPYTAPELLFFAKRYKAATTECQQAADKAACLPK 181	RA	RT
DB	147 AKCTAQNEAFQAGFLHVARPHPPYGPPELLYADKTAVTECAADDKGACTLPK 206	RA	RT
QY	182 LDELDEGKASSAKQKUCAKSLQKGERAKWAVARLSORPKAFAEYSKLVDLTKY 241	RA	RT
DB	207 LDALKERKAVLAVSRQLKCSMFKGERAKWAVARMSQTFPADEITKLADLTQK 266	RC	SEQUENCE OF 477-551 FROM N.A.
QY	242 HTECGGDLLEADDRADLAKYICNQDSSKLLKQCGPLEKSHIAETENDMPAD 301	RC	SEQUENCE OF 477-551 FROM N.A.
DB	267 TQECCGDLLEADDRADLAKYICNQDSSKLLKQCGPLEKSHIAETENDMPAD 326	RC	SEQUENCE OF 477-551 FROM N.A.
QY	302 LPSIAADPESKDVCKNAYAEDQVLEGNFLPYTARHPDYSVVLILAKTYETTLKCC 361	RC	SEQUENCE OF 477-551 FROM N.A.
DB	327 ITPATDNEVEDKDVCKNAYAEDQVLEGNFLPYTARHPDYSVVLILAKTYETTLKCC 386	RC	SEQUENCE OF 477-551 FROM N.A.
QY	362 AAADPHECYAKVDFEDEKPLVYEPONLTKONCEFLFGOLGEKEYKONVALIYRVTKQVPOVSTP 421	RC	SEQUENCE OF 477-551 FROM N.A.
DB	387 AEADPHACGHHYDFEDEKPLVYEPONLYASNCNCLYELFGQFAVIYRVTKQVPOVSTP 446	RC	SEQUENCE OF 477-551 FROM N.A.
QY	422 TIVYVSPRLKGVSQCKKHPAKSMPCADYXVWVNLQCVLHEKPTVSDRVTKCCTESL 481	RC	SEQUENCE OF 477-551 FROM N.A.
DB	447 TLYVAAARSILGRYTHCCALPEKKLPCVTDYLSAUNRVCLLHEKPTVSEQYTKCGSGL 506	RC	SEQUENCE OF 477-551 FROM N.A.
QY	482 VNRPCFSALEYDTEVPKFNAETFTPHADICLSEBEKQIKQTALYEVKHKPKATK 541	RC	SEQUENCE OF 477-551 FROM N.A.
DB	507 VERPCFSALPDETFPKFKAETFTPHADICLSEBEKQIKQTALYEVKHKQFATE 566	RC	SEQUENCE OF 477-551 FROM N.A.
QY	542 EQLKAVMDDEAFAVEKCKADDKETCPAEGKKLYVAAASQAL 583	RC	SEQUENCE OF 477-551 FROM N.A.

"Mouse liver protein database; a catalog of proteins detected by two-dimensional gel electrophoresis";

Electrophoresis 13:970-991 (1992).

-1- FUNCTION: serum albumin, the main protein of plasma, has a good binding capacity for water, Ca^{2+} , Na^{+} , K^{+} , fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

-1- SUBCELLULAR LOCATION: Secreted.

CC :- TISSUE SPECIFICITY: Plasma.
 CC :- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC :- SIMILARITY: Contains 3 albumin domains.

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CC DR EMBL; AJ011413; CAR09617.1; -
 DR EMBL; M16111; AAA37190.1; -
 DR EMBL; X13060; CRA31458.1; -
 DR EMBL; AK010025; BAB26650.1; -
 DR PIR; AU05139; AU05139.
 DR HSSP; P02768; 1E7B.
 DR SWISS-2DPAGE; P07724; MOUSE.
 DR SGD; MGI:87991; ALB1.
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00073; transport_prot; 3.
 DR ProDom; PRO00802; SERUMALBUMIN.
 DR PRODOM; PRO02486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR SWISS-PROT; PS00242; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24 BY SIMILARITY.
 FT CRAN1 25 608 SERUM ALBUMIN.
 FT DOMAIN 25 205 ALBUMIN 1.
 FT DOMAIN 212 397 ALBUMIN 2.
 FT DOMAIN 404 595 ALBUMIN 3.
 FT METAL 27 27 COPPER.
 FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 289 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 462 BY SIMILARITY.
 FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.
 FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 FT CONFLICT 27 27 H > D (IN REF. 5).
 FT CONFLICT 33 33 H > D (IN REF. 5).
 FT CONFLICT 41 41 Q > I (IN REF. 5).
 SQ SEQUENCE 608 AA; 68692 MW; 29277/FEED3a1B4 CRC64;

Query Match 76.6%; Score 2378; DB 1; Length 608;
 Best Local Similarity 72.4%; Pred. No. 2.1e-14;
 Matches 422; Conservative 80; Mismatches 81; Indels 0; Gaps 0;

Db 205 KLDGVVKEKALVYSTRQRMKCSSNQKTFGERAKAWAVALSRQFPNDAEETKIAATDITK 264
 241 VHTTECHGDLCEADDRADLAKYICENQDSSSKLKECEPKLEKSHCIAEVENDEMA 300
 265 VNECECHGDLCEADDRAEALAKYMCENQATSSKLQTCDCPKLKAHLCESEVHDITMPA 324
 301 DPLSLADFEVSKDVKYNAEAKDVLGMLYEARHDPDSYVLLRLAKTYETLKC 360
 325 DLPAIAADFEVQEKVYNAEAKDVFELGTFLYEXSRRDPDSYVLLRLAKKYBATELKC 384
 361 CAAADPPECTAKVDFEPLVPEPQNTLQKNCLEPQEKEYFQNALVLYTRVTPQVST 420
 385 CAEANPAPCAGTGYLAEPQPLVPEPKVNUYKNCNDLYKEGYFQNALVLYTRVTPQVST 444
 421 PTIIVEVSRNLGKVGSCKCKHPEAKMCAEDEYLTSVNLNOLCVLHEKTPVSDRVTKCCES 480
 445 PIVLVEARNLGRVGTCKCTLPEQDRLCIVEDYLSAILRVCLHEKTPVSEHVTKCCSGS 504
 481 LYNNRCPFSALEYDTYVPEKEVAAETTFHADICLSEKERQKOTALVLYKHKPKAT 540
 505 LYNNRCPFSALEYDTYVPEKEVAAETTFHADICLPEKEQKOTALVLYKHKPKAT 564
 541 KEGQLKAVMDDEAATYKCKAADDKETCFQAFERGKLVAAASQAAI 583
 565 AEQLKTYMDDEAQDFDTCKKAADKDTFSTEGPNLVYTRCKDAL 607

RESULT 13
 ALBU_CHICK
 ID ALBU_CHICK STANDARD; PRT; 615 AA.
 AC P19121;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-PEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Gallinidae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 RA Cassady A.I., Salkeld C.K., Baverstock P., Wallace J.C.;
 RA Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
 RN [2];
 RP SEQUENCE OF 1-28 FROM N.A.
 RA Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deelev R.G.;
 RA MEDLINE-83161037; PubMed-6187737;
 RA "The 5' noncoding and flanking regions of the avian very low density
 RT apolipoprotein II and serum albumin genes. Homologies with the egg
 RT white protein genes";
 RA J. Biol. Chem. 258:4556-4564 (1983).
 RN [3];
 RP SEQUENCE OF 19-30.
 RX MEDLINE-78019943; PubMed-911327;
 RA Rosen A.M., Geller D.M.;
 RP "Chicken microsomal albumin: amino terminal sequence of chicken
 RT proalbumin";
 RL Biochem. Biophys. Res. Commun. 78:1660-1666 (1977).
 CC :- FUNCTION: Serum albumin, the main protein of plasma, has a good
 CC binding capacity for water, Ca(2+), Na(+), K(+) , fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidal osmotic pressure of blood.
 CC :- SUBCELLULAR LOCATION: Secreted.
 CC :- TISSUE SPECIFICITY: Plasma.
 CC :- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC :- SIMILARITY: Contains 3 albumin domains.
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CC EMBL; X60688; CAA43098; 1..
 DR PROTEIN; Y00381; CAA23680; 1..
 FT PROPEP; S15371; ABCES.
 DR HSSP; P02768; 1E7B.
 DR InterPro; IPI000264; Serum_albumin.
 DR PF00273; PR0002; TRANSPORT_Prot; 3.
 DR PRINTS; PR0002; SERUMALBUMIN.
 DR PRODOM; PD00486; Serum_albumin; 1..
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 DR KW Metal-binding; Lipid-binding; Repeat; Signal; copper.
 FT SIGNRL; 1..18
 FT PROPEP; 19..23
 FT CHAIN; 24..615 SERUM_ALBUMIN.
 FT DOMAIN; 24..209 ALBUMIN_1..
 FT DOMAIN; 216..401 ALBUMIN_2..
 FT DOMAIN; 408..599 ALBUMIN_3..
 FT METAL; 30..30 COPPER (BY SIMILARITY).
 FT DISULFID; 80..89 BY SIMILARITY.
 FT DISULFID; 102..118 BY SIMILARITY.
 FT DISULFID; 117..128 BY SIMILARITY.
 FT DISULFID; 152..197 BY SIMILARITY.
 FT DISULFID; 196..205 BY SIMILARITY.
 FT DISULFID; 228..274 BY SIMILARITY.
 FT DISULFID; 273..281 BY SIMILARITY.
 FT DISULFID; 293..307 BY SIMILARITY.
 FT DISULFID; 306..317 BY SIMILARITY.
 FT DISULFID; 344..389 BY SIMILARITY.
 FT DISULFID; 388..397 BY SIMILARITY.
 FT DISULFID; 420..466 BY SIMILARITY.
 FT DISULFID; 465..476 BY SIMILARITY.
 FT DISULFID; 489..505 BY SIMILARITY.
 FT DISULFID; 504..515 BY SIMILARITY.
 FT DISULFID; 512..512 BY SIMILARITY.
 FT DISULFID; 586..595 BY SIMILARITY.
 FT CARBOHYD; 500..500 N-LINKED (GLCNAC, . .) (POTENTIAL).
 FT CONFLICT; 24..24 F->M (BCN REF. 3).
 SQ SEQUENCE; 615 AA; 69918 MW; E59E4BECB6C6 CRC64;

RESULT 14

FETA_PANTHER STANDARD; PRT; 609 AA.

ID FETA_PANTHER ID 028789; AC 028789; DT 28-FEB-2003 (Rel. 41, Created) DT 28-FEB-2003 (Rel. 41, Last annotation update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DE Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein). DE DE APP. DE APP. OS Pan_troglodytes (Chimpanzee). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. OC NCBI_TaxID=9598; RN [1] RP SEQUENCE FROM N.A. RX MDDLINE=903245; PubMed=755731; RA Nishio, H.; Gibbs, P.E.; Minghetti, P.P.; Zielinski, R.; Dugaiczky, A.; RT The chimpanzee alpha-fetoprotein encoding gene shows structural similarity to that of gorilla but distinct differences from that of RT human." RL Gene 162:213-220(1995). CC -1- FUNCTION: Binds copper, nickel, and fatty acids as well as, and CC -1- bilirubin less well than, serum albumin. Only a small percentage CC -1- (less than 2%) of the human AFP shows estrogen-binding properties. CC -1- SUBUNIT: Dimeric and trimeric forms have been found in addition CC -1- to the monomeric form. CC -1- SUBCELLULAR_LOCATION: Secreted. CC -1- TISSUE_SPECIFICITY: Plasma. Synthesized by the fetal liver and CC -1- yolk sac. CC -1- BELONGS_TO THE ALB/APP/YDB FAMILY. CC -1- SIMILARITY: Contains 3 albumin domains.

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CC EMBL; U21916; AA01641; 1..
 DR PIR; JC4256;
 DR HSSP; P02768; 1E7B.
 DR InterPro; IPR00264; Serum_albumin.
 DR PRINTS; PR00273; transport_prot; 3..
 DR PRODOM; PD002486; Serum_albumin; 1..
 DR PROSITE; PS00103; ALBUMIN; 2..
 DR Glycoprotein; Sulfation; Repeat; Metal-binding; Copper; Nickel; Signal; 1..18 BY SIMILARITY.
 FT CHAIN; 19..609 ALPHA-FETOPROTEIN.
 FT DOMAIN; 20..205 ALBUMIN 1..
 FT DOMAIN; 212..397 ALBUMIN 2..

QY 3 HKSEVAHREFKDGEENFKALVIAFAQYIQLQQCPFEDBEVLYNEVTEFAKTCYADESAENC 62
 DB 30 HKSEVAHREFKDGEENFKALVIAFAQYIQLQQCPFEDBEVLYNEVTEFAKTCYADESAENC 62
 QY 63 DKSPLHFLGDKLCTVATLREYGENWADCAKOBPERNECTLQHDDNPNLPR-LYRPEVD 121
 DB 90 SKPPLSILIDECQVERKLRSYGAADCSSKAQDENECFLSFVQSDDFVQYQPSAD 149
 QY 122 YMCATAFHNEETLKKVLYETARPHPYTAPELFAKRYKAATTECCQAAKAKLPK 181
 DB 150 VTCQYQDNRVSPHLGHTYSARPPFVYAPALTSAYDEPHALQSCCKESDVGACIDTK 209
 QY 182 LDELDREDEKASSAKQRLKCSLQKGERAFKAMAVRLSORPKAFAEVSKLYDILKV 241
 DB 210 EIVMREKAGVSYKQYFCGTLKQKDRYFQARQLYSKYKAPFSEVYHUSIGV 269
 QY 242 HTECCHGDOLIECADRDLAKTICYNODSISKKLKECERPLERSHCTADEVENDPAD 301
 DB 270 HKCECCEGDAVECMDDMARMNSNLCSQDFTSGKIKDCCEKREVESQCMEEAEFDEPAD 329
 QY 302 LPSLAADFVEKSYCKVNAEKAQDVKLGFMLEYKARHPDYSVWLLRLAKTYETTELKCC 361
 DB 330 LPSLVEKYTEDKEYCKSFEAGHDAFMAEFTYEVSRRHPEFSTQLMRTAKYESTLKECC 389

FT	DOMAIN	404	595	ALBUMIN 3, COOPER AND NICKEL (BY SIMILARITY).	DE	Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein).
FT	METAL	22	22	BY SIMILARITY.	DE	AFP.
FT	DISULFID	99	114	BY SIMILARITY.	GN	Homo sapiens (Human).
FT	DISULFID	113	124	BY SIMILARITY.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	DISULFID	148	193	BY SIMILARITY.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
FT	DISULFID	192	201	BY SIMILARITY.	OC	NCB_ TaxID=9606;
FT	DISULFID	224	270	BY SIMILARITY.	OX	[1]
FT	DISULFID	269	277	BY SIMILARITY.	RN	RN
FT	DISULFID	289	303	BY SIMILARITY.	RX	SEQUENCE FROM N.A.
FT	DISULFID	302	313	BY SIMILARITY.	RX	MEDLINE=83273664; PubMed=6192439;
FT	DISULFID	384	393	BY SIMILARITY.	RA	Gibbs P.E.M., Zielinski R., Boyd C., Dugaiczyk A.;
FT	DISULFID	416	462	BY SIMILARITY.	RA	McEvoy J.H., Michaelides K., Hansen L.P., Ferguson-Smith M.,
FT	DISULFID	461	472	BY SIMILARITY.	RA	Tilgman S., Krunkauf R., Tuddenham E.G.D.;
FT	DISULFID	485	501	BY SIMILARITY.	RT	"A G->A substitution in an BNF I binding site in the human alpha-fetoprotein gene is associated with hereditary persistence of alpha-fetoprotein (HFAP).";
FT	DISULFID	500	511	BY SIMILARITY.	RT	a complete sequence of the human alpha-fetoprotein gene.;"
FT	DISULFID	538	583	BY SIMILARITY.	RL	Proc. Natl. Acad. Sci. U.S.A. 80:4604-4608(1983).
FT	DISULFID	582	591	BY SIMILARITY.	RN	[2]
FT	CARBONYD	442	N-LINKED (GLCNAC. . .) (POTENTIAL).	RN	RN	
FT	CARBONYD	251	N-LINKED (GLCNAC. . .) (POTENTIAL).	RN	SEQUENCE FROM N.A.	
SQ	SEQUENCE	609 AA;	68741 MW;	C032987CAD08672B CRC64;	RX	MEDLINE=7185438; PubMed=2436661;
QY		3	HKSE---VAHRFKDLGKLCVATLRETYGEMADCCAKQEPERNCFLOHKDDNP-NLPLRIV	57	RX	SEQUENCE OF 1-28 FROM N.A.
Db		22	HREYGAISLDISQCTAINEILDLATIIFQQFQDAYTKEVSKMVKDALTAEIKPTGDE	81	RX	MEDLINE=93278385; PubMed=7684942;
QY		58	SACNCDLSLHTLFQGKLCVATLRETYGEMADCCAKQEPERNCFLOHKDDNP-NLPLRIV	116	RA	Gibbs P.E.M., Zielinski R., Hansen L.P., Ferguson-Smith M.,
Db		82	QSACGLNQLPAFELBLREKEIKEYGH-SDCCSQESEGRHNCFLAHKKPTEPPTQ	140	RA	McEvoy J.H., Michaelides K., Hansen L.P., Ferguson-Smith M.,
QY		117	RPEVDVINCTAHDNEETEKKLYKEIARRHYTFPELLEFAKRYKAFATCCQADRAA	176	RA	Tilgman S., Krunkauf R., Tuddenham E.G.D.;
Db		141	VPEPVTCSEAYEADTDRFUNKTYEIARRHDFELVPTILWARYDKLIPSCCKRAENAYE	200	RA	"A G->A substitution in an BNF I binding site in the human alpha-fetoprotein gene is associated with hereditary persistence of alpha-fetoprotein (HFAP).";
QY		177	CLPKLDELRDEGKASSAKTORLKASLOQKPERAKAWARYLQSRQPKAFAEVSLVT	236	RA	a complete sequence of the human alpha-fetoprotein deduced from
Db		201	CFTQKAATVYKELTRESSLNQHACAVKNEGTRTQATVTKLSQTKTKYTFEQLV	260	RA	RT
QY		237	DLTKVHTTECCHSDLLECADDRADLAKTYCERQDSISSKLLKECCQPKLEKSHCTAEVEND	296	RA	RT
Db		261	DVAHVHEHCCRSDVLDCLQDGEKMTSICSQDTSNKTCECKLTLERGQCTHAEND	320	RA	"Human alpha-fetoprotein primary structure: a mass spectrometric study";
QY		297	EMPADLPSLAADFVEKPKYRREKDYF35	356	RA	RT
Db		321	EKPGGLSPNLNRLFGDRDFQSSGEKNIFLASFREYSRHLQASVLRVARGIQEL	380	RA	RT
QY		357	LEKCCAAADPHRCYAKVEDRFKPKVPEPQNLQKNCLEFQGEYKTYKQNLVRYTKYK	416	RA	RT
Db		381	LEKQFOTENPLQDQGEELQKTYQEQALAKRSGFLQKLGYQNALPLVTKAP	440	RA	RT
QY		417	QVSEPTLVYEVSRNLQVGSKCCKPEAKRMPQAEDYLSTVNLQCLVHLHEKTPVSDRVPKC	476	RA	RT
Db		441	QLTSESELMAITRMAATAQCCQSEDKLACGEAADLIGHICHTHETPVNGVGC	500	RA	RT
QY		477	CTPESLWNRCPCSALEDEVYFPEKQFADLICLSETERQIKKQPAFLVKEK	536	RA	RT
Db		501	CTSSYANTRCPCSLIVYDEYVPPDAFSQDKEFHDLCQAGYALPMQKQFLINIVKSK	560	RA	RT
QY		537	PKATKEQLKAVMDDFAAVFEVKCQKADDKETCFAEQSKKIVAAQALG	585	RA	RT
Db		561	PQTEEEQLEVNIDFSSLLERKCCGQEQEVCPAEQSKLTSKTAHGV	609	RA	"Alpha fetoprotein: structure and expression in man and inbred mouse strains under normal conditions and liver injury.";
RESULT	15				RL	RT
FEFA_HUMAN					RL	RT
ID	FETAL_HUMAN				RL	RT
AC	PO22771				RL	RT
DT	21-JUL-1986 (Rel. 01, Created)				RL	RT
DT	21-JUL-1986 (Rel. 01, Last sequence update)				RL	RT
DT	28-FEB-2003 (Rel. 41, Last annotation update)				RL	RT

flanking region";
 RL J. Biol. Chem. 260:5055-5060(1985).
 RN [10]
 METAL-BINDING
 RP MEDLINE:79001617; PubMed=80265;
 RX Aoyagi Y., Ikenaka T., Ichida F.;
 RA "Copper(II)-binding ability of human alpha-fetoprotein.";
 RT Cancer Res. 38:3483-3486(1978).
 RL Cancer Res. 39:5571-3574(1979).
 RN [11]
 RP BILLIRUBIN-BINDING
 RX MEDLINE:80001710; PubMed=89900;
 RA Aoyagi Y., Ikenaka T., Ichida F.;
 RT "Alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-
 binding ability";
 RT binding ability";
 RL Cancer Res. 39:5571-3574(1979).
 RN [12]
 RP SULFATION
 RX MEDLINE:86042625; PubMed=2414772;
 RA Liu M.C., Yu S., SY J., Redman C.M., Lipmann F.;
 RT "Tyrosine sulfation of proteins from the human hepatoma cell line
 RT Hep2.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
 CC -1- FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND
 CC BILLIRUBIN LESS WELL THAN, SERUM ALBUMIN. ONLY A SMALL PERCENTAGE
 CC (LESS THAN 2%) OF THE HUMAN AFP SHOWS ESTROGEN-BINDING PROPERTIES.
 CC -1- SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION
 CC TO THE MONOMERIC FORM.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: PLASMA. SYNTHESIZED BY THE FETAL LIVER AND
 CC YOLK SAC.
 CC -1- DEVELOPMENTAL STAGE: OCCURS IN THE PLASMA OF FETUSES MORE THAN 4
 CC WEEKS OLD, REACHES THE HIGHEST LEVELS DURING THE 12TH-16TH WEEK OF
 CC GESTATION, AND DROPS TO TRACE AMOUNTS AFTER BIRTH. THE SERUM LEVEL
 CC IN ADULTS IS USUALLY LESS THAN 40 NG/ML. AFP OCCURS ALSO AT HIGH
 CC LEVELS IN THE PLASMA AND ASCITIC FLUID OF ADULTS WITH HEPATOMA.
 CC -1- PTM: INDEPENDENT STUDIES SUGGEST HETEROGENEITY OF THE AMINO-
 CC TERMINAL SEQUENCE OF THE MATURE PROTEIN AND OF THE CLEAVAGE SITE
 CC OF THE SIGNAL SEQUENCE.
 CC -1- PTM: SULFATED.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/YDB FAMILY.
 CC -1- SIMILARITY: Contains 3 albumin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is not
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 CC -----
 DR M10949; AAA51674.1;
 DR EMBL; M10950; AAA51675.1;
 DR Y01514; CRA24758.1;
 DR M16110; AAB58754.1;
 DR EMBL; Z19532; CAA79592.1;
 DR PIR; A26244; PPHU.
 DR HSP; P02768; LE7B.
 DR Glycosidase; P02771; -
 DR Sialia-2D PAGE; P02771; -
 DR Genew; HGNC:3117; AFP.
 MN: 104150; -
 DR Interpro; IPR00264; Serum albumin.
 DR Pfam; PF00273; transport protein; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR Prodom; PD002486; Serum albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00120; ALBUMIN; 2.
 KW Glycoprotein; Sulfation; Repeat; Metal-binding; Copper; Nickel;
 KW Signal; Polymorphism.
 FT SIGNAL 1 18
 FT CHAIN 19 609 ALPHA-FETOPROTEIN.
 FT DOMAIN 20 205 ALBUMIN 1.
 FT DOMAIN 212 397 ALBUMIN 2.

FT DOMAIN 404 595 ALBUMIN 3.
 FT METAL 22 22 COPPER AND NICKEL.
 FT DISULFID 99 114
 FT DISULFID 113 124
 FT DISULFID 148 193
 FT DISULFID 192 201
 FT DISULFID 224 270
 FT DISULFID 269 277
 FT DISULFID 289 303
 FT DISULFID 302 313
 FT DISULFID 384 393
 FT DISULFID 416 462
 FT DISULFID 461 472
 FT DISULFID 485 501
 FT DISULFID 500 511
 FT DISULFID 538 583
 FT DISULFID 582 591
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .).
 FT VARIANT 570 570 /FTID=CAR_000070.
 A -> G (in disnp:1057173).
 /FTID=VAR_012049.
 SO SEQUENCE 609 AA; 68677 MW: 4D1E45B20E1C2D4F CRC64;
 Query Match 40.3%; Score 1249.5%; DB 1; Length 609;
 Best Local Similarity 39.9%; Pred. No. 4.e-7;
 Matches 235; Conservative 116; N mismatches 231; Indels 7; Gaps 3;
 QY 3 HKSE ---VAHFKDQGEENFKALVLIQAFTQOQFEDEVKLVNEFATKTCAYDE 57
 Db 22 HRFNEYGTASILDYQCTAEISLADATIFQAFQVQATVKEVSKMVKDALTATEKPKGDE 81
 QY 58 SAENCDKSLHHTFGDKLCTVATLRETYGMADCAKOPERNECFLQHKDDNP-NLPRLV 116
 Db 82 QSSGCLENQDPAFEEQHBERLLEYGH-SDCOSQSEGEHNCFLAHKRTPTASIPIFQ 140
 QY 117 RPEVDVACTAFAHNEEFLKLYELTARHPPYTAPELFFAKRYKAFTTECQAAADKA 176
 Db 141 VPEPYTSCAYEEDETFMNRKPYTETARSHFLYIAPTILWAAARDKILPSCCAENAEV 200
 QY 177 CLLPKDDELDREGASSAKQRKUCASLQFGERAFKAWAVALSORPKFAEVSKLIV 236
 Db 201 CEFQTRAAFTYKELRESSLINQHACAMKNGTTRQTAQITWKLQSKPTVNFIEQKILV 260
 QY 237 DLTKVHTECCHGDLIECADDRADLAKTICENODOSISSKLKECEPKLKSHTAEVEND 296
 Db 261 DVAHYHTEHRCGVDLQDGDKNSYTCSQDPLSNKITECKLTLLERGQCTIHAEND 320
 QY 297 EMPADIPSIAADFYESKDVCKNYAFAKDFGMFLYEXARRHPPDSVYVLLRLAKTYETT 356
 Db 321 EKEPEGSPLNREFLGDQDENFGSGEKNIFLASEPHESSRHPPOLAVSTLRYAKGQEL 380
 QY 357 LEKCAAADPHEYAKTDEKFPLVPEPQNLINONEFEEQGEKTFQNALLYTRKVP 416
 Db 381 LEKCPOTENPLECQDGEEELOKYQESQALAKRSCEFGKQIGEYLYQNAFLVATYTKKAP 440
 QY 417 QSYSTPLVVEYRSNRIGKYGSKCCKHPEAKMPCADYLSSVVLNOLCYLHKTPTPSDRTYK 476
 Db 441 QLTSSSLMATTMAATAATCQLSSEDKLIACGGAAIDILIGHCLIREHTP/NPGQCL 500
 QY 477 CTESLYNRPFCSALEYDETYPKFNAETFPHADICLSEKEROIKKOTALVLYKHK 536
 Db 501 CTSSYANRPFCSSLVYDTEVPPAFSDDKFIHKDLCQAGQVALQTMQEOFILNLVYKQK 560
 QY 537 PKATREQLKAVMDFAATFVERCRADDKETCFREBGAKLYVASQALGL 585
 Db 561 PQITREQLEAVIADFSSGLERCCQGQEQEVCFAREGOKLISKTRALG 609

Search completed: August 31, 2003, 16:33:47
 Job time : 28 secs

421 PTLVEVRNLGKVGSCKCKPHEAKRMPADYLUSVVIQVLYHEPTPSDRVRCCCTS 480
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 364 ELLIFTR- ITZASRCCVEYTDKLKPCGYDEVLGICORHQSSINVNCQCCNS 422
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 481 LYNRPCPSALLEDETYPKERNAFTFHADICLSEKERQIKQTALVELVHKPRAT 540
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 423 YALRSLCITSIGDEKEVPTESADLFTEDLCHAQDKLQERKQOMIVLYVHKPNIT 482
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 541 KEOLKAVMDFAFEVKCCRADKETFEAEKGKLVASAQAL 583
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 483 KEQJQTVGGFQTMEKCKRADHEACFGEGPKLVASQAL 525

RESULT 6						
MJU5	PRELIMINARY;	PRT;	609 AA.			
Q8MUT5	PRELIMINARY;	PRT;	609 AA.			
Q8MUT5;						
01-OCT-2002 (TREMBLrel. 22, Created)						
01-OCT-2002 (TREMBLrel. 22, Last sequence update)						
01-MAR-2003 (TREMBLrel. 23, Last annotation update)						
Alpha-fetoprotein.						
Canis familiaris (Dog).						
Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;						
Canis familiaris (Dog).						
Canis, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						
Canis, Carnivora; Fissipedia; Canidae; Canis.						
NCBI_TAXID=9615;						
[1]	SEQUENCE FROM N.A.					
Furnichi M., Neo S., Hisasue M., Tsuchiya R., Watanabe M.,						
Hishizaki K., Hisamatsu S., Yamada T.;						
"Canine alpha-fetoprotein cDNA."						
Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.						
EMBL; AB08978; BAC0513.1;						
InterPro; IPR000264; Serum albumin.						
InterPro; IPR00273; transport_prot; 3.						
PRINTS; PRO00802; SERMALBUMIN.						
PRINTS; PRO00486; Serum albumin; 1.						
SMART; SM00103; ALBUMIN; 3.						
PROSITE; PS00212; ALBUMIN; 2.						
SEQUENCE 609 AA;						
68782 MW;						
BE4B8250C5AF2AFO CRC64;						
Query Match 40.0%; Score 1242; DB 6; Length 609;						
Best Local Similarity 40.5%; Pred. No. 2.7e-85;						
Matches 231; Conservative 113; Mismatches 225; Indels 2; Gaps 2;						
16 EENFKALVLIAPAQYIQQCQPPEDEVLYNEVTEFATIVCADESAEBCNDCESLHTLFGKLIC 75						
40 EMNIVDLATIIFQAQQYEAQTYKEYSKAYKDILTVIKSTGSEQPGCLNOLPAFEBIC 99						
76 TVALVRETYGENADCAKOPBNECQHQKD-DNPFLPPLRVPRPVYDNTCAAHDNDEET 134						
100 HEKEISEKYG-LADCO3QREERENCFIAHKKAAPPSIPPEQVAEPVTSCKAYEENDM 158						
135 LKXLYTEARHPPYTAPELLEFKAARYKAATTECCQAAADKAACLPLKDLDEKGKASSA 194						
159 MNRYIYEARPPFLYTAPELLEFKAARYKAATTECCQAAADKAACLPLKDLDEKGKASSA 218						
195 KORUKCASLQFGERAKFANAVARLQSQRPKAFAEVSKLYDTLTKHRECCHGDLLECA 254						
219 LNOQIATMNRGPRERFLTVKLSQRFSKANFTEQKLVLYDAHIEBCCGRGNVLECL 278						
255 DDRADLARYICINODSSKLIKEQPKRPLSHCAEVENDPAPLSLADFVSK 314						
279 QDGKEMTYSICSQDLSSKTIADCCKLPLLEGQCTIHAENDGKPEGSPNRLFELRD 338						
315 VCKNAYAAEKDVYIIGMFLYEEYARRHEDYSVYLLRLAKTYENTLEKCCAADPHECYAKVF 374						
339 FNQSSREKDLPMARITYEYSRRIKTLKAVPWLVRKGQELLERCSQSENPLCQKGE 398						
375 DEFPPLVPEPQNLKONCEPEQLEYEYKFQNALVYRKTKVPOVSTPLVENSRLRKG 434						
399 EELRKYIQESQNLAKTSQGFLQGYLQVYIQLNAFLPEMLATRKAATA 458						
OS Ambystoma maculatum (spotted salamander).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;						
OC Ambystoma.						
ALB.						
GN OS Ambystoma maculatum (spotted salamander).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;						
NCBI_TAXID=43114;						
OX RN [1]	SEQUENCE FROM N.A.					
RC TISSUE=Liver;						
RA Harverfield E.V., Uzzell T., Spolsky C.M., Bazzartseren B.;						
RT "Serum albumin of the mole salamanders <i>Ambystoma maculatum</i> and <i>Ambystoma texanum</i> ."						
RL Submitted (DB0-1999) to the EMBL/GenBank/DBJ databases.						
DR EMBL; AF217183; AAL56646.1; -.						
DR Interpro; IPR000364; Serum_albumin.						
DR Pfam; PF00273; transport_prot; 3.						
DR PRINTS; PRO00802; SERMALBUMIN.						
DR PRODOM; PD002486; Serum_albumin; 1.						
DR SMART; SM00103; ALBUMIN; 3.						
DR PROSITE; PS00212; ALBUMIN; 2.						
KW SIGNAL.						
FT CHAIN 1 24 POTENTIAL.						
FT SIGNAL 25 626 SERUM ALBUMIN.						
SEQUENCE 626 AA; 70677 MW; 9D66F5F174C23F CRC64;						
Query Match 40.0%; Score 1242; DB 13; Length 626;						
Best Local Similarity 40.1%; Pred. No. 2.8e-89; Pred. No. 2.8e-89;						
Matches 237; Conservative 110; Mismatches 238; Indels 6; Gaps 3;						
QY 1 DAHKSEVAHFRKL---GEENFKALVLIAPAQYIQQCQPPEDEVLYNEVTEFAKTYAD 56						
Db 28 EGHYDNPPLPQHPLIGLPMIGVGDNSKGLVLAASQDMPLCPYEEHQLRVEDYQMLADLCKG 87						
QY 57 ESAENCDKESLHLTFLGDKLCIVATRETYGEMDCAQEQPERNECLQHDDN-PNLRL 115						
Db 68 ARHANCARSPTMIIIDELCKPENAEKPKYPPHQBCCKKDPRHKCEVEMKMANHEELTY 147						
QY 116 VRPEVDYNTCAHDFNDEETFLKKLYTEIARRHPPYAFAPLKEKTYAFKRAFECQAAOKA 175						
Db 148 VRPAEQICKDAENQGPGLARYIIMLAIGHPMVIAUQGLAQRDGTIVSHCKDQVTEA 207						
QY 176 A-CLPKLDELDEGGKASSAKQRLKCAQSLQKPCERAKVAVARLQSQRPKAFAEYSKL 234						
Db 208 GQCQNDKMPKPEHQEVYCALQKINCYLQDQPERATAYKQDQPLASFENYQII 267						
QY 235 VTDLTKVHTECQHGDLCADDRADLAKTYCENQDSISLKECCQKPLLEKSHIAVE 294						
Db 268 VPDTVHLHOTCGDDNACMIEURKLTAKICEKFDEATHIKECCDKPLLERSACTIRLP 327						
QY 295 NDEMPADLPSLAADFETESKDVCKNYAAEKDVYGMFLYEEYARRHEDYSVYLLRLAKTYE 354						
Db 328 NDQPADSPKYPHDDPEVCKLYTEGDTGFRYECARRHODYSPMLURMGGYE 387						

QY	355 TLEKCCAAADPHECYAKVDEFKKPPLYEEPONLIKONGCELEQOLGEYKFONALLYRTEKK 414	Db	399 EEELEKQYIQQESALARSKCGLFQKIGETYLQNAFLIVAYTAKAPOLTPPELMALTRCMAAT 453
Db	388 EFTKKCCAEEHNRCLATEESELSKKEESESSYTLLTNGCALDKLKLKYLEFQNLIFKTYAR 447	QY	434 GSKCCKHPEAKRMPCAEDYLSVWLNQLCYLHFKTPYSDRTKCCTESTVNRRPCFSALEV 493
QY	415 VPQVSEPTLVEVSRLNGLKRGSKCCKHPEAKRMPCAEDYLSVWLNQLCYLHFKTPYSDRT 474	Db	459 GAACCHLSSDROLACRGAAADLIGQOLTRHEMPINPGQCCOTSSANRPCFCSSLV 518
Db	448 MPALSESSLRITKSMITIGERKCHRPEDQMTCTCEGGGGTYGQICMKQKTTFVNEKVA 507	QY	494 DETYPKPEKNAETFTPHADICLTSEKERQIKQTALVLYKHKRKPATEKEQIKAVMDDEAA 553
QY	475 KCTTSLVNRRPCFSALEYDETPKPEKNAETFTPHADICLTSEKERQIKQTALVLYK 534	Db	519 DETYPPPFSDDKFTHKDLCQAGVLAQTMQOFILNLYKQKQQTIEQLEPAVLADESG 578
Db	508 QCCSHSISSTQTPCFSSALPDEYVPPPLSVAFNDELCTSEPEQOSKQVTLIRMLK 567	QY	554 FVERKCRADDKETCFBEGSKLVVASQALGL 585
QY	535 HKPKATKEOKLAVMDFAAVERCKKCATDDEKTCFAEEGKLYAAQSAAQLG 585	Db	579 LLERCCGCGEQEYVCFEEGPALISKTRASLGV 610
Db	568 QIPHMHTDEQLKTCVVNFPAVVDQCKADNHNECFALEGAKLIDACKAILAV 618		
RESULT 8			
Q8M7J6	PRELIMINARY; PRT; 610 AA.	Q8UW06	PRELIMINARY; PRT; 624 AA.
ID	08M7J6;	AC	Q8UW06;
AC	08M7J6;	DT	01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Created)	DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DE	Serum albumin precursor.
DE	Alpha-fetoprotein.	GN	ALB.
OS	Sus scrofa (Pig).	OS	Ambystoma texanum (Shallowmouth salamander).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	OC	Ambystomatidae; Ambystomoidea; Salamandroidea;
OX	NCBI_TAXID=9823;	OX	NCBI_TAXID=8304;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	Kim J.G., Nonnenmacher D., Vallet J.L., Christensen R.K.;	RA	Harverfield E.V., Uzzell T., Spolsky C.M., Bazarartseren B.;
RT	"Mapping of the porcine alpha-fetoprotein (AFP) gene to SSC8."	RT	"Serum albumin of the mole salamanders Ambystoma maculatum and
RL	Submitted (UN-2002) to the EMBL/GenBank/DBJ databases.	RT	Ambystoma texanum."
DR	EMBL; AF517770; AAM66710.1;	RL	Submitted (DSC-1999) to the EMBL/GenBank/DBJ databases.
DR	InterPro; IPR000264; Serum_albumin.	DR	EMBL; AF21718; AAL56645.1;
DR	PFam; PF00213; transport_prot; 3.	DR	InterPro; IPR00264; Serum_albumin.
DR	PRINTS; PR002486; Serum_ALBUMIN.	DR	PFam; PF00273; transport_prot; 3.
DR	ProDom; PD002486; Serum_ALBUMIN.	DR	PRINTS; PR00812; SERUM_ALBUMIN.
DR	ProDom; PD002486; Serum_ALBUMIN; 1.	DR	ProDom; PD002486; Serum_albumin; 1.
DR	SMART; SM00103; ALBUMIN; 3.	DR	SMART; SM00103; ALBUMIN; 3.
DR	PROSITE; PS00212; ALBUMIN; 2.	DR	PROSITE; PS00112; ALBUMIN; 1.
SQ	SEQUENCE 610 AA; 68624 MW; C985BEAD44963D5E CRC64;	KW	SIGNAL.
Query Match	39.3%; Score 1218.5; DB 6; Length 610;	FT	1 24
Best Local Similarity	39.7%; Pred. No 1.9e-87;	CHAIN	25
Matches	227; Conservative 117; Mismatches 225; Indels 3; Gaps 3;	FT	624
Db	40 EMMNUVDAITFQVQEATYKVNQVAKYDLYTVEKSTGSEOPAGLNOVSYFLEEC 99	SEQUENCE	624 AA; 70321 MW; DEB0833BF4953EE7 CRC64;
QY	16 EENFKALVLTAFQYLQOCOPFEDHVKLYNETEFAFKTCAADEAENCDKSLSHTLEFDKLC 75	Query Match	35.0%; Score 1087; DB 13; Length 624;
Db	40 EMMNUVDAITFQVQEATYKVNQVAKYDLYTVEKSTGSEOPAGLNOVSYFLEEC 99	Best Local Similarity	37.7%; Pred. No. 4.3e-77;
Db	76 TVALTRELTYGEMDCCAKOEPEERNECFLQHDDNP-NILPLRVPEVDYCTAFTHDNEEF 134	Matches	214; Conservative 102; Mismatches 240; Indels 12; Gaps 5;
QY	100 HESEIPEXYG-LSHCOSOSEERHNCFLARKKAASASTIPFQVPEPFTSKAYEENRELF 158	QY	14 LGEENFKALVLTAFQYLQOCOPFEDHVKLYNETEFAFKTCAADEAENCDKSLSHTLEFDK 73
Db	135 LKLYLYTARRHPPFYAAPLLFAPKRYKAATTECCQAADCLPKLDEERDECKASSA 194	Db	45 IGVEFTAKALAMALFQMSLISKPCPHFQQVQRVNMFDADLCSRGAHKGDCGSVMTLINE 104
QY	159 KQRLKCASLQKFGERAKWAVARSORPFAEEFKTCAVAFKQVLAETTLEKTLVYKETTLEKRELESSI 218	QY	74 LCTYATLRLTYGEMDCCAKOEPEERNECFLQHDDNP-NILPLRVPEVDYCTAFTHDNEE 132
Db	195 KQRLKASLQKFGERAKWAVARSORPFAEEFKTCAVAFKQVLAETTLEKTLVYKETTLEKRELESSI 218	Db	105 ICKTFENPEKTFPHGCKKEDPERHKFIEKSTDFEKERTETVYKPSFQICKDHEAEND 164
QY	219 LQHMCMTYARQEGARTFRATIVTQLSKQFKPANFEIQLVLDVATHHEECGRGAVLCL 278	QY	133 TFLKLYEVIAARRHPPFYAAPLLFAPKRYKAATTECCQAADCLPKLDEERDEGKA 191
Db	255 DDRADLAKTYCENQDSISSKLKECEKCP-LLEKSHCIAEVENDMPADLPSLAADFVES 313	Db	165 EFLGHYIKVASSHTMPAIISETLRFDGVSHCKDKEATVQCLSERMAKHEVEH 224
QY	279 QDARERWVSYCSQDPLTSKIAECKLPLTIELGCQIHAENDKPEGLSPNLNRFGLER 338	QY	192 SSAKORLKCASLQKFGERAKWAVARSORPFAEEFKTCAVAFKQVLAETTLEKTLVYKETTLEKRELESSI 251
Db	314 DVCKNYAKADYFLGMLFELYARHPDYSVWLLILAKTYETTLEKCCAAADPHECYAKV 373	Db	225 VCAYQKHNCYIQLNEFRLRASKAAHCSKPHAFENTRLTDGTHLHOTCGGDM 284
QY	339 DFNOLSSREKULSMARTEFEYSRRHPLKLAVENTLVKAGYQELLEKCSQSONPLEQDKG 398	QY	252 ECADDRAEAKYCEQDSSKLUKECEKPKLEKSHCIAEVENDMPADLPSLAADFVE 311
Db	374 FDFEKPLVYEEPONLIKONGCELEQOLGEYKFONALLYRTEKKVQVSPTLYEVSRNLGRV 433	Db	285 ACMARMLKLTQTCEK-----KKCEKPKLVESECIVRLPDEKADLSPVRYFD 336
QY	399 EEELEKQYIQQESALARSKCGLFQKIGETYLQNAFLIVAYTAKAPOLTPPELMALTRCMAAT 453	QY	312 SKDVCKNYAERKDFLGMLFELYARHPDYSVWLLILAKTYETTLEKCCAAADPHECYA 371

337	DEPCKKEFKERSDAFMGRFLCDAKIHPHESAAELNTRIASGLEGAYKCCAGEAINECTIA	396	Db	395 EELQKHEESEQLSKOSCALYQTLGDKYKLQNLFLIGYTKAPOLTSALIDLTGKMSVIA 454
372	KVDEKFPLVPEPQNLKONCEFEQGEYKFQNALLVREYTKPVQYSTPLVVEYSRNLG 431	Qy	435 SKCKHPEAKRMPAEDLSSWVLNQCLVLYHEKTPSDRVTKCCTESTLYNRPFCSALEYD 494	
397	KFETELRHEESESKTKLKTGCALEKYGPHQNTMIVRTGILPSSDATTLYTKTEI 456	Db	455 SPCQTSSEVRTSGCGEADITGHCIRNAPNSGSHCONSTSNSRRLCTSFRLD 514	
432	KVSSCKKXHPKAKPMPCAEDLYSVLNQCLVLYHEKTPV-SDRVTKCCTESTLYNRPFCSA 490	Qy	495 ETYVPEKKEFNAETTFHADCTLSEKERQKTKTALYEVLYKHKPKEQKAVMDFAAF 554	
457	NTGQKCCKLPEQDQMCSEGGLAVFQIC-ONQKPFPENEKLAHCCDSDLSFTPCFAA 515	Db	515 ETYAPPFSEKFTHKDLCQAHGKALQTMQELINLYKQDPELTBEQLAATFDSL 574	
491	LEYDEYYPKEFNAETTFHADCTLSEKERQKTKTALYEVLYKHKPKEQKAVMD 550	Qy	555 VPKCKADKETCFEEGKLYVASSQALGL 585	
516	LTVDETYPPAPVTAESFNPDFEPTSPADLQAKOTFLMHLVTHPKTIDEQVTTISEK 575	Db	575 LIRKCKAQDQEVCTEEGPKLISKTRDALGV 605	
551	FAAFVEKCKKADKETCFEEGKLYVAA 578			
576	ELAMCGQCKRADQNECPATEGALIVEA 603			
	RESULT 11			
	Q8BK56	PRELIMINARY;	PRT;	605 AA.
	ID	Q8BK56		
	AC	Q8BK56;		
	DT	01-MAR-2003	(TRIMBREL 23, Created)	
	DT	01-MAR-2003	(TRIMBREL 23, Last sequence update)	
	DT	01-MAR-2003	(TRIMBREL 23, Last annotation update)	
	DE	Alpha-fetoprotein precursor.		
	OS	Mus musculus (Mouse)		
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	OC	Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus;		
	NCBI_TaxID	10090;		
	RN	[1]		
	RR	SEQUENCE FROM N_A		
	RC	STRAIN=57BL/6J; TISSUE=Placenta, and Extraembryonic tissue;		
	RX	PubMed=12466851;		
	RA	The FANTOM Consortium;		
	RA	The RIKEN Genome Exploration Research Group Phase I & II Team;		
	RT	Analysis of the mouse transcriptome based on functional annotation of		
	RT	60,770 full-length cDNAs";		
	RL	Nature 420:563-573 (2002).		
	DR	EMBL; AK076197; BAC56249.1; -.		
	SQ	SEQUENCE 605 AA; 67409 MW; CF3509A9EC141610 CRC64;		
		Query Match Score 1076; DB 11; Length 605;		
		Best Local Similarity 35.6%; Pred. No. 3.1e-76; Mismatches 242; Indels 6; Gaps 3;		
		Matches 203; Conservative 120; Mismatches 242; Indels 6; Gaps 3;		
	QY	16 EENEKALVYLIAFAQYLQQCPFEDHHVKNVNEYTEFKTCKVADESAENCDKSLSHTLFGDKLC 75		
	DB	40 EKVNLSTATIITQFVPEATEEE---VNKMTSDVLAAMKKNSGDGCLESQSLVFLDEIC 95		
	QY	76 TVATLRLTYGMAEDCQAKPERNECFQHQHDDNP-NLPLPVLVPEVDYCTAFHNEETF 134		
	DB	96 HEPELSKYG-LSGCCSQSGVVERHQCLLARKTAAVSFPEPESCKAHEERNRAYF 154		
	QY	135 LKLYLTYEADDCQAKQSPPEREECFQHQHDDNP-NLPLPVLVPEVDYCTAFHNEETF 134		
	DB	155 MNFIFIIVSRNPNHIAPIPLSIAAQDVKVLLACRDNKECQTRASTAKEIREGSM 214		
	QY	195 KQFLKASLQKGERAKWAVARLSSQRPKAEEFKVADKAACLJPKDLEDEKASSA 194		
	DB	215 LNEHVCVSIRKFESRNQQTTLKSLQKLTBANEFTQIQKALAYAHTHEECQGNSLECL 274		
	QY	255 DDEADLARYICENDPSISSEKLRKCECPPLERKSHGTAEVENDMPADLPSLAADPVESESD 314		
	DB	275 QDQEKTWVTYICSQNLLSKIAECKPELQGFLTIIHENGKPEELSLAPSQPLGDRN 334		
	QY	315 VCKNYAFAKDVGMFLYEXYARHPDYSWVLLRLAKTYETTLEKCGAADPHECYAKF 374		
	DB	335 FAQFSSEKTMFMSFLHEYSRTHPNLPVSYTIRAKTQETLEKCSQSGNLPGQDQDN 394		
	QY	375 DEPKPLVPEPONLKQNCFLPELQGEYKFKONALVRYTKPVYSTPLVYRSNLKGYV 434		
	DB	395 EELQKHEESEQLSKOSCALYQTLGDKYKLQNLFLIGYTKAPOLTSALIDLTGKMSVIA 454		
	QY	435 SKCKHPEAKRMPAEDLYSVLNQCLVLYHEKTPSDRVTKCCTESTLYNRPFCSALEYD 494		

532	QY	LVKKPATAKQQLKAVADDEAFAPEKKCQKADKETTGFPEBKKLVASQAL 583
354	Db	VVCKPATAKQQLKAVADDEAFAPEKKCQKADKETTGFPEBKKLVASQAL 405

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Job time: 111 secs